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OM protein - protein search, using sw model

Run on: November 17, 2005, 22:29:18 ; Search time 75 Seconds
(without alignments)
72.195 Million cell updates/sec

Title: US-09-745-008-14

Perfect score: 78

Sequence: 1 RQLPKRMGGSYRC 14

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A Geneseq_16Dec04:*

1: Geneseqp19808:*

2: Geneseqp19908:*

3: Geneseqp20008:*

4: Geneseqp20018:*

5: Geneseqp20028:*

6: Geneseqp20038:*

7: Geneseqp20038b:*

8: Geneseqp20048:*

.Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	78	100.0	14	7 ADC21513	Adc21513 T. cruzi
2	78	100.0	21	7 ADC21512	Adc21512 T. cruzi
3	78	100.0	1162	7 ADC21533	Adc21533 T. cruzi
4	67.5	86.5	45	7 ADC21511	Adc21511 T. cruzi
5	45	57.7	433	7 ABO79949	ABO79949 Pseudomon
6	43	55.1	164	7 ABO81408	ABO81408 Pseudomon
7	43	55.1	164	7 ABO71869	ABO71869 Pseudomon
8	43	55.1	223	7 ABO70073	ABO70073 Pseudomon
9	43	55.1	545	7 ABO81671	ABO81671 Pseudomon
10	42.5	54.5	1107	7 ABO62373	ABO62373 Klebsiell
11	42	53.8	30	2 AAW89049	AAW89049 Polypepti
12	42	53.8	30	4 ABB51214	ABB51214 Human sec
13	42	53.8	30	6 ABO45471	ABO45471 Novel hum
14	42	53.8	30	7 ABO26951	ABO26951 Protein a
15	42	53.8	339	4 ABB68550	ABB68550 Drosophil
16	42	53.8	419	7 ABO68753	ABO68753 Pseudomon
17	41	52.6	189	4 AAU42341	AAU42341 Propionib
18	41	52.6	189	6 ABM38860	ABM38860 Propionib
19	41	52.6	212	5 ABB75629	ABB75629 Human end
20	41	52.6	492	7 ABO71785	ABO71785 Pseudomon
21	41	52.6	511	7 ABO69945	ABO69945 Pseudomon
22	41	52.6	556	7 ABO73842	ABO73842 Pseudomon
23	41	52.6	564	8 ADN17932	ADN17932 Bacterial
24	41	52.6	595	7 ABO68723	ABO68723 Pseudomon
25	40.5	51.9	235	2 AAR05328	AAR05328 Rat tumou

26	40.5	51.9	235	2 AAR05996	AAR05996 Rat tumou
27	40.5	51.9	235	5 AAU10546	AAU10546 Rat tumou
28	40	51.3	61	8 ADO47390	ADO47390 Human neu
29	40	51.3	92	3 AAG33234	AAG33234 Zee maya
30	40	51.3	138	3 AAG33233	AAG33233 Zee maya
31	40	51.3	151	4 ABG16755	ABG16755 Novel hum
32	40	51.3	230	4 AAG98324	AAG98324 Escherich
33	40	51.3	230	6 ABU14845	ABU14845 Protein e
34	40	51.3	259	7 ADB64149	ADB64149 Human pro
35	40	51.3	279	7 ABM74436	ABM74436 DNA clone
36	40	51.3	299	4 ABB76024	ABB76024 Human pro
37	40	51.3	299	8 ADO47379	ADO47379 Human neu
38	40	51.3	302	6 ABUS2331	ABUS2331 Human GPC
39	40	51.3	302	6 ABUS2330	ABUS2330 Human GPC
40	40	51.3	302	8 ADL23995	ADL23995 Human NOV
41	40	51.3	302	8 ADL23997	ADL23997 Human NOV
42	40	51.3	303	7 ABO74011	ABO74011 Pseudomon
43	40	51.3	355	7 ABO78680	ABO78680 Pseudomon
44	40	51.3	362	7 ABO81880	ABO81880 Pseudomon
45	40	51.3	419	7 ABO79741	ABO79741 Pseudomon

ALIGNMENTS

RESULT 1

ADC21513
ID ADC21513 standard; peptide; 14 AA.

XX ADC21513;

DT 18-DEC-2003 (first entry)

XX T. cruzi trans-sialidase, TS, neurotrophic peptide C14.

DE Trans-sialidase; TS; neurotrophic peptide; interleukin-6;

KW IL-6 secretion inducing peptide; neuron; glial cell; trophic support;

KW ciliary neurotrophic factor; CNTF; leukaemia inhibitory factor; LIF;

KW neurotrophic lateral sclerosis; Alzheimer's disease; Parkinson's disease;

KW Huntington's disease; Chagas' disease; peripheral neuropathy; palsy;

KW multiple sclerosis; stroke; brain trauma; spinal cord trauma;

KW peripheral nerve trauma.

XX Trypanosoma cruzi.

OS US2002137667-A1.

PN 26-SEP-2002.

PD 20-DEC-2000; 2000US-00745008.

XX 20-DEC-1999; 99US-0172881P.

XX (TUFT) UNIV TUFTS.

XX Chuenkova M, Persira MA;

XX WPI; 2003-786654/74.

XX T. cruzi trans-sialidase derived neurotrophic and interleukin-6 secretion inducing peptides, useful in the treatment of neuronal degeneration caused for example by Chagas' disease.

PS Claim 5; SEQ ID NO 14; 79pp; English.

XX The invention relates to a T. cruzi trans-sialidase (TS) derived neurotrophic peptide appearing as ADC21513 or ADC21511 called C44 and C14, or its variant, and an interleukin-6 (IL-6) secretion inducing peptide appearing as ADC21531 called TR-1 (terminal repeat 1). Also included are a composition comprising the peptides, fusion protein comprising the peptides and a fusion partner, a composition comprising the fusion protein and a physiological acceptable carrier, providing trophic support for neurons or glial cells in a mammal (comprising

CC administering a therapeutically effective amount of T. cruzi trans-
 CC sialidase (TS) or a neurotrophic variant) and stimulating (M3) the
 CC secretion of IL-6 (interleukin-6) in a mammal comprising administering TS
 CC or an IL-6 inducing variant. The fusion partner comprises a mammalian
 CC neurotrophic factor which is ciliary neurotrophic factor (CNTF) or
 CC leukaemia inhibitory factor (LIF). The peptides are useful in providing
 CC trophic support for neurons and glial cells in a mammal suffering a
 CC condition selected from: amyotrophic lateral sclerosis, Alzheimer's
 CC disease, Parkinson's disease, Huntington's disease, Chagas' disease,
 CC peripheral neuropathy, palsies, multiple sclerosis, stroke, brain trauma,
 CC spinal cord trauma and peripheral nerve trauma, and in stimulating the
 CC secretion of IL-6. The present sequence represents a trans-sialidase
 CC neurotrophic peptide.
 XX
 SQ Sequence 14 AA;

Query Match 100.0%; Score 78; DB 7; Length 14;
 Best Local Similarity 100.0%; Pred. No. 1.1e-06;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RQRLPKRMGGSYRC 14
 |||||
 Db 1 RQRLPKRMGGSYRC 14

RESULT 2

ADC21512
 ID ADC21512 standard; peptide; 21 AA.

AC ADC21512;

DT 18-DEC-2003 (first entry)

DE T. cruzi trans-sialidase, TS, neurotrophic peptide CFN1.

Trans-sialidase; TS; neurotrophic peptide; interleukin-6;
 IL-6 secretion inducing peptide; neuron; glial cell; trophic support;
 ciliary neurotrophic factor; CNTF; leukaemia inhibitory factor; LIF;
 amyotrophic lateral sclerosis; Alzheimer's disease; Parkinson's disease;
 Huntington's disease; Chagas' disease; peripheral neuropathy; palsy;
 multiple sclerosis; stroke; brain trauma; spinal cord trauma;
 peripheral nerve trauma.

OS Trypanosoma cruzi.

PN US2002137667-A1.

PD 26-SEP-2002.

PF 20-DEC-2000; 2000US-00745008.

PR 20-DEC-1999; 99US-0172881P.

PA (TUFT) UNIV TUFTS.

PI Chuenkova M, Pereira MA;

DR WPI; 2003-786654/74.

T. cruzi trans-sialidase derived neurotrophic and interleukin-6 secretion
 inducing peptides, useful in the treatment of neuronal degeneration
 caused for example by Chagas' disease.

Example 1; SEQ ID NO 13; 79pp; English.

The invention relates to a T. cruzi trans-sialidase (TS) derived
 neurotrophic peptide appearing as ADC21513 or ADC21511 called C44 and
 C14, or its variant, and an interleukin-6 (IL-6) secretion inducing
 peptide appearing as ADC21531 called TR-1 (terminal repeat 1). Also
 included are a composition comprising the peptides, fusion protein
 comprising the peptides and a fusion partner, a composition comprising
 the fusion protein and a physiological acceptable carrier, providing
 trophic support for neurons or glial cells in a mammal (comprising

CC administering a therapeutically effective amount of T. cruzi trans-
 CC sialidase (TS) or a neurotrophic variant) and stimulating (M3) the
 CC secretion of IL-6 (interleukin-6) in a mammal comprising administering TS
 CC or an IL-6 inducing variant. The fusion partner comprises a mammalian
 CC neurotrophic factor which is ciliary neurotrophic factor (CNTF) or
 CC leukaemia inhibitory factor (LIF). The peptides are useful in providing
 CC trophic support for neurons and glial cells in a mammal suffering a
 CC condition selected from: amyotrophic lateral sclerosis, Alzheimer's
 CC disease, Parkinson's disease, Huntington's disease, Chagas' disease,
 CC peripheral neuropathy, palsies, multiple sclerosis, stroke, brain trauma,
 CC spinal cord trauma and peripheral nerve trauma, and in stimulating the
 CC secretion of IL-6. The present sequence represents a trans-sialidase
 CC neurotrophic peptide.
 XX
 SQ Sequence 21 AA;

Query Match 100.0%; Score 78; DB 7; Length 21;
 Best Local Similarity 100.0%; Pred. No. 1.7e-06;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RQRLPKRMGGSYRC 14
 |||||
 Db 1 RQRLPKRMGGSYRC 14

RESULT 3

ADC21533
 ID ADC21533 standard; protein; 1162 AA.

AC ADC21533;

DT 18-DEC-2003 (first entry)

DE T. cruzi trans-sialidase, TS, clone 7P.

Trans-sialidase; TS; neurotrophic peptide; interleukin-6;
 IL-6 secretion inducing peptide; neuron; glial cell; trophic support;
 ciliary neurotrophic factor; CNTF; leukaemia inhibitory factor; LIF;
 amyotrophic lateral sclerosis; Alzheimer's disease; Parkinson's disease;
 Huntington's disease; Chagas' disease; peripheral neuropathy; palsy;
 multiple sclerosis; stroke; brain trauma; spinal cord trauma;
 peripheral nerve trauma.

OS Trypanosoma cruzi.

PN US2002137667-A1.

PD 26-SEP-2002.

PF 20-DEC-2000; 2000US-00745008.

PR 20-DEC-1999; 99US-0172881P.

PA (TUFT) UNIV TUFTS.

PI Chuenkova M, Pereira MA;

DR WPI; 2003-786654/74.

T. cruzi trans-sialidase derived neurotrophic and interleukin-6 secretion
 inducing peptides, useful in the treatment of neuronal degeneration
 caused for example by Chagas' disease.

Disclosure; SEQ ID NO 34; 79pp; English.

The invention relates to a T. cruzi trans-sialidase (TS) derived
 neurotrophic peptide appearing as ADC21513 or ADC21511 called C44 and
 C14, or its variant, and an interleukin-6 (IL-6) secretion inducing
 peptide appearing as ADC21531 called TR-1 (terminal repeat 1). Also
 included are a composition comprising the peptides, fusion protein
 comprising the peptides and a fusion partner, a composition comprising
 the fusion protein and a physiological acceptable carrier, providing

CC trophic support for neurons or glial cells in a mammal (comprising
 CC administering a therapeutically effective amount of T. cruzi trans-
 CC sialidase (TS) or a neurotrophic variant) and stimulating (M3) the
 CC secretion of IL-6 (interleukin-6) in a mammal comprising administering TS
 CC or an IL-6 inducing variant. The fusion partner comprises a mammalian
 CC neurotrophic factor which is ciliary neurotrophic factor (CNTF) or
 CC leukaemia inhibitory factor (LIF). The peptides are useful in providing
 CC trophic support for neurons and glial cells in a mammal suffering a
 CC condition selected from: amyotrophic lateral sclerosis, Chagas' disease,
 CC disease, Parkinson's disease, Huntington's disease, stroke, brain trauma,
 CC peripheral neuropathy, palsies, multiple sclerosis, stroke, brain trauma,
 CC spinal cord trauma and peripheral nerve trauma, and in stimulating the
 CC secretion of IL-6. The present sequence represents trans-sialidase clone
 CC 7F.
 XX
 SQ Sequence 1162 AA;
 Query Match 100.0%; Score 78; DB 7; Length 1162;
 Best Local Similarity 100.0%; Pred. No. 0.00011; Indels 0; Gaps 0;
 Matches 14; Conservative 0; Mismatches 0;
 QY 1 RQRLPKRMGGSYRC 14
 |||||
 Db 379 RQRLPKRMGGSYRC 392
 RESULT 4
 ADC21511
 ID ADC21511 standard; peptide; 45 AA.
 XX
 AC ADC21511;
 XX
 DT 18-DEC-2003 (first entry)
 DE
 DE T. cruzi trans-sialidase, TS, neurotrophic peptide C44.
 XX
 KW Trans-sialidase; TS; neurotrophic peptide; interleukin-6;
 KW IL-6 secretion inducing peptide; neuron; glial cell; trophic support;
 KW ciliary neurotrophic factor; CNTF; leukaemia inhibitory factor; LIF;
 KW amyotrophic lateral sclerosis; Alzheimer's disease; Parkinson's disease;
 KW Huntington's disease; Chagas' disease; peripheral neuropathy; palsy;
 KW multiple sclerosis; stroke; brain trauma; spinal cord trauma;
 KW peripheral nerve trauma.
 XX
 OS Trypanosoma cruzi.
 XX
 PN US2002137667-A1.
 XX
 XX 26-SEP-2002.
 XX
 PF 20-DEC-2000; 2000US-00745008.
 XX
 PF 20-DEC-1999; 99US-0172881P.
 PR
 XX (TUFT) UNIV TUFTS.
 PA
 XX Chuenkova M, Pereira MA;
 PI
 XX WPI; 2003-786654/74.
 DR
 XX
 PT T. cruzi trans-sialidase derived neurotrophic and interleukin-6 secretion
 PT inducing peptides, useful in the treatment of neuronal degeneration
 PT caused for example by Chagas' disease.
 PT
 PS Claim 4; SEQ ID NO 12; 79pp; English.
 XX
 CC The invention relates to a T. cruzi trans-sialidase (TS) derived
 CC neurotrophic peptide appearing as ADC21513 or ADC21511 called C44 and
 CC C14, or its variant, and an interleukin-6 (IL-6) secretion inducing
 CC peptide appearing as ADC21531 called TF-1 (terminal repeat 1). Also
 CC included are a composition comprising the peptides, fusion protein
 CC comprising the peptides and a fusion partner, a composition comprising
 CC the fusion protein and a physiological acceptable carrier, providing

CC trophic support for neurons or glial cells in a mammal (comprising
 CC administering a therapeutically effective amount of T. cruzi trans-
 CC sialidase (TS) or a neurotrophic variant) and stimulating (M3) the
 CC secretion of IL-6 (interleukin-6) in a mammal comprising administering TS
 CC or an IL-6 inducing variant. The fusion partner comprises a mammalian
 CC neurotrophic factor which is ciliary neurotrophic factor (CNTF) or
 CC leukaemia inhibitory factor (LIF). The peptides are useful in providing
 CC trophic support for neurons and glial cells in a mammal suffering a
 CC condition selected from: amyotrophic lateral sclerosis, Chagas' disease,
 CC disease, Parkinson's disease, Huntington's disease, stroke, brain trauma,
 CC peripheral neuropathy, palsies, multiple sclerosis, stroke, brain trauma,
 CC spinal cord trauma and peripheral nerve trauma, and in stimulating the
 CC secretion of IL-6. The present sequence represents a trans-sialidase
 CC neurotrophic peptide.
 XX
 SQ Sequence 45 AA;
 Query Match 86.5%; Score 67.5; DB 7; Length 45;
 Best Local Similarity 93.3%; Pred. No. 0.00028;
 Matches 14; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
 QY 1 RQRLP-KRMGGSYRC 14
 |||||
 Db 24 RQRLPLKRMGGSYRC 38
 RESULT 5
 AB079949
 ID AB079949 standard; protein; 433 AA.
 XX
 AC AB079949;
 XX
 DT 29-JUL-2004 (first entry)
 DE
 DE Pseudomonas aeruginosa polypeptide #12124.
 XX
 KW Bacterial infection; Pseudomonas aeruginosa infection; antibacterial.
 KW Pseudomonas aeruginosa.
 OS
 PN US6551795-B1.
 XX
 PD 22-APR-2003.
 XX
 PF 18-FEB-1999; 99US-00252991.
 XX
 PR 18-FEB-1998; 98US-0074788P.
 PR 27-JUL-1998; 98US-0094190P.
 XX
 XX (GENO-) GENOME THERAPEUTICS CORP.
 PA
 PI Rubenfield MJ, Nolling J, Deloughery C, Bush D;
 XX
 DR WPI; 2003-615309/58.
 DR N-PSDB; ABD13520.
 XX
 PT Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide,
 PT useful as molecular targets for diagnostics, prophylaxis and treatment of
 PT pathological conditions resulting from bacterial infection.
 XX
 PS Disclosure; SEQ ID NO 28695; 455pp; English.
 XX
 CC The invention relates to Pseudomonas aeruginosa polypeptides and the
 CC polynucleotides encoding them. The sequences are useful in diagnosis and
 CC therapy of pathological conditions, as molecular targets for diagnostics,
 CC prophylaxis and treatment of pathological conditions resulting from a
 CC bacterial infection, for evaluating a compound, such as a polypeptide,
 CC for the ability to bind a P. aeruginosa nucleic acid, as components of
 CC effective antibacterial targets, as targets for antibacterial drugs,
 CC including anti-P. aeruginosa drugs, as templates for recombinant
 CC production of P. aeruginosa-derived peptides or polypeptides, as target
 CC components for diagnosis and/or treatment of P. aeruginosa-caused
 CC infection, and in detection of P. aeruginosa sequences or other sequences

CC of Pseudomonas species using biochip technology. Sequences AB067826-
 CC AB084396 represent P. aeruginosa polypeptides of the invention. Note: The
 CC sequence data for this patent did not form part of the printed
 CC specification but was obtained in electronic format from USPTO at
 CC seqdata.uspto.gov/sequence.html
 XX
 SQ Sequence 433 AA;

Query Match 57.7%; Score 45; DB 7; Length 433;
 Best Local Similarity 64.3%; Pred. No. 28;
 Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
 Qy 1 RQRLPKRMGGSYRC 14
 Db 251 RRLPVRPGGPGRC 264
 |||||
 |||||

RESULT 6
 ABO81408
 ID ABO81408 standard; protein; 164 AA.
 XX
 AC ABO81408;
 XX
 DT 29-JUL-2004 (first entry)
 XX
 DE Pseudomonas aeruginosa polypeptide #13583.
 XX
 KW Bacterial infection; Pseudomonas aeruginosa infection; antibacterial.
 XX
 OS Pseudomonas aeruginosa.
 XX
 PN US6551795-B1.
 XX
 PD 22-APR-2003.
 XX
 PF 18-FEB-1999; 99US-00252991.
 XX
 PR 18-FEB-1998; 98US-0074788P.
 PR 27-JUL-1998; 98US-0094190P.
 XX
 PA (GENO-) GENOME THERAPEUTICS CORP.
 XX
 PI Rubenfield MJ, Nolling J, Deloughery C, Bush D;
 XX
 WPI; 2003-615309/58.
 DR N-PSDB; ABD14979.

XX Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide,
 XX useful as molecular targets for diagnostics, prophylaxis and treatment of
 XX pathological conditions resulting from bacterial infection.
 XX
 PS Disclosure; SEQ ID NO 30154; 455pp; English.
 XX
 CC The invention relates to Pseudomonas aeruginosa polypeptides and the
 CC polynucleotides encoding them. The sequences are useful in diagnosis and
 CC therapy of pathological conditions, as molecular targets for diagnostics,
 CC prophylaxis and treatment of pathological conditions resulting from a
 CC bacterial infection, for evaluating a compound, such as a polypeptide,
 CC for the ability to bind a P. aeruginosa nucleic acid, as components of
 CC effective antibacterial targets, as targets for antibacterial drugs,
 CC including anti-P. aeruginosa drugs, as templates for recombinant
 CC production of P. aeruginosa-derived peptides or polypeptides, as target
 CC components for diagnosis and/or treatment of P. aeruginosa-caused
 CC infection, and in detection of P. aeruginosa sequences or other sequences
 CC of Pseudomonas species using biochip technology. Sequences AB067826-
 CC AB084396 represent P. aeruginosa polypeptides of the invention. Note: The
 CC sequence data for this patent did not form part of the printed
 CC specification but was obtained in electronic format from USPTO at
 CC seqdata.uspto.gov/sequence.html
 XX
 SQ Sequence 164 AA;

Query Match 55.1%; Score 43; DB 7; Length 164;
 Best Local Similarity 50.0%; Pred. No. 24;
 Matches 7; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Best Local Similarity 50.0%; Pred. No. 24;
 Matches 7; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
 Qy 1 RQRLPKRMGGSYRC 14
 Db 73 RRRMPRRSGPATRC 86
 |||||
 |||||

RESULT 7
 ABO71869
 ID ABO71869 standard; protein; 164 AA.
 XX
 AC ABO71869;
 XX
 DT 29-JUL-2004 (first entry)
 XX
 DE Pseudomonas aeruginosa polypeptide #4044.
 XX
 KW Bacterial infection; Pseudomonas aeruginosa infection; antibacterial.
 XX
 OS Pseudomonas aeruginosa.
 XX
 PN US6551795-B1.
 XX
 PD 22-APR-2003.
 XX
 PF 18-FEB-1999; 99US-00252991.
 XX
 PR 18-FEB-1998; 98US-0074788P.
 PR 27-JUL-1998; 98US-0094190P.
 XX
 PA (GENO-) GENOME THERAPEUTICS CORP.
 XX
 PI Rubenfield MJ, Nolling J, Deloughery C, Bush D;
 XX
 WPI; 2003-615309/58.
 DR N-PSDB; ABD05440.

XX Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide,
 XX useful as molecular targets for diagnostics, prophylaxis and treatment of
 XX pathological conditions resulting from bacterial infection.
 XX
 PS Disclosure; SEQ ID NO 20615; 455pp; English.
 XX
 CC The invention relates to Pseudomonas aeruginosa polypeptides and the
 CC polynucleotides encoding them. The sequences are useful in diagnosis and
 CC therapy of pathological conditions, as molecular targets for diagnostics,
 CC prophylaxis and treatment of pathological conditions resulting from a
 CC bacterial infection, for evaluating a compound, such as a polypeptide,
 CC for the ability to bind a P. aeruginosa nucleic acid, as components of
 CC effective antibacterial targets, as targets for antibacterial drugs,
 CC including anti-P. aeruginosa drugs, as templates for recombinant
 CC production of P. aeruginosa-derived peptides or polypeptides, as target
 CC components for diagnosis and/or treatment of P. aeruginosa-caused
 CC infection, and in detection of P. aeruginosa sequences or other sequences
 CC of Pseudomonas species using biochip technology. Sequences AB067826-
 CC AB084396 represent P. aeruginosa polypeptides of the invention. Note: The
 CC sequence data for this patent did not form part of the printed
 CC specification but was obtained in electronic format from USPTO at
 CC seqdata.uspto.gov/sequence.html
 XX
 SQ Sequence 164 AA;

Query Match 55.1%; Score 43; DB 7; Length 164;
 Best Local Similarity 50.0%; Pred. No. 24;
 Matches 7; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
 Qy 1 RQRLPKRMGGSYRC 14
 Db 73 RRRMPRRSGPATRC 86
 |||||
 |||||

RESULT 8

ABO70073
ID ABO70073 standard; protein; 223 AA.
AC ABO70073;
DT 29-JUL-2004 (first entry)
DE Pseudomonas aeruginosa polypeptide #2248.
KW Bacterial infection; Pseudomonas aeruginosa infection; antibacterial.
OS Pseudomonas aeruginosa.
PN US6551795-B1.
PD 22-APR-2003.
PF 18-FEB-1999; 99US-00252991.
PR 18-FEB-1998; 98US-0074788P.
PR 27-JUL-1998; 98US-0094190P.
XX (GENO-) GENOME THERAPEUTICS CORP.
XX Rubenfield MJ, Nolling J, Deloughery C, Bush D;
XX WPI; 2003-615309/58.
XX N-PSDB; ABD01644.
XX Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide,
XX useful as molecular targets for diagnostics, prophylaxis and treatment of
XX pathological conditions resulting from bacterial infection.
XX Disclosure; SEQ ID NO 18819; 455pp; English.
XX The invention relates to Pseudomonas aeruginosa polypeptides and the
XX polynucleotides encoding them. The sequences are useful in diagnosis and
XX therapy of pathological conditions, as molecular targets for diagnostics,
XX prophylaxis and treatment of pathological conditions resulting from a
XX bacterial infection, for evaluating a compound, such as a polypeptide,
XX for the ability to bind a P. aeruginosa nucleic acid, as components of
XX effective antibacterial targets, as targets for antibacterial drugs,
XX including anti-P. aeruginosa drugs, as templates for recombinant
XX production of P. aeruginosa-derived peptides or polypeptides, as target
XX components for diagnosis and/or treatment of P. aeruginosa-caused
XX infection, and in detection of P. aeruginosa sequences or other sequences
XX of Pseudomonas species using biochip technology. Sequences ABO67826-
XX ABO84396 represent P. aeruginosa polypeptides of the invention. Note: The
XX sequence data for this patent did not form part of the printed
XX specification but was obtained in electronic format from USPTO at
XX seqdata.uspto.gov/sequence.html
XX Sequence 223 AA;
Query Match 55.1%; Score 43; DB 7; Length 223;
Best Local Similarity 58.3%; Pred. No. 32;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
QY 1 RORLPKRMGGSY 12
DB 183 RQRIPRRGRH 194
RESULT 9
ABO81671
ID ABO81671 standard; protein; 545 AA.
XX ABO81671;
XX 29-JUL-2004 (first entry)
XX Pseudomonas aeruginosa polypeptide #13846.
DE

KW Bacterial infection; Pseudomonas aeruginosa infection; antibacterial.
XX Pseudomonas aeruginosa.
XX US6551795-B1.
XX 22-APR-2003.
XX 18-FEB-1999; 99US-00252991.
XX 18-FEB-1998; 98US-0074788P.
XX 27-JUL-1998; 98US-0094190P.
XX (GENO-) GENOME THERAPEUTICS CORP.
XX Rubenfield MJ, Nolling J, Deloughery C, Bush D;
XX WPI; 2003-615309/58.
XX N-PSDB; ABD15242.
XX Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide,
XX useful as molecular targets for diagnostics, prophylaxis and treatment of
XX pathological conditions resulting from bacterial infection.
XX Disclosure; SEQ ID NO 30417; 455pp; English.
XX The invention relates to Pseudomonas aeruginosa polypeptides and the
XX polynucleotides encoding them. The sequences are useful in diagnosis and
XX therapy of pathological conditions, as molecular targets for diagnostics,
XX prophylaxis and treatment of pathological conditions resulting from a
XX bacterial infection, for evaluating a compound, such as a polypeptide,
XX for the ability to bind a P. aeruginosa nucleic acid, as components of
XX effective antibacterial targets, as targets for antibacterial drugs,
XX including anti-P. aeruginosa drugs, as templates for recombinant
XX production of P. aeruginosa-derived peptides or polypeptides, as target
XX components for diagnosis and/or treatment of P. aeruginosa-caused
XX infection, and in detection of P. aeruginosa sequences or other sequences
XX of Pseudomonas species using biochip technology. Sequences ABO67826-
XX ABO84396 represent P. aeruginosa polypeptides of the invention. Note: The
XX sequence data for this patent did not form part of the printed
XX specification but was obtained in electronic format from USPTO at
XX seqdata.uspto.gov/sequence.html
XX Sequence 545 AA;
Query Match 55.1%; Score 43; DB 7; Length 545;
Best Local Similarity 61.5%; Pred. No. 81;
Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
QY 1 RORLPKRMGGSY 13
DB 56 RSRLPRRAGGEVR 68
RESULT 10
ABO62373
ID ABO62373 standard; protein; 1107 AA.
XX ABO62373;
XX 29-JUL-2004 (first entry)
XX Klebsiella pneumoniae polypeptide seqid 8890.
XX Recombinant expression vector; transcription regulatory element;
XX Klebsiella pneumoniae protein; antibacterial; vaccine.
XX Klebsiella pneumoniae.
XX US6610836-B1.
XX 26-AUG-2003.
PD

PF	27-JAN-2000; 2000US-00489039.	XX	97US-00488933P.
XX		XX	97US-0048894P.
PR	29-JAN-1999; 99US-0117747P.	PR	97US-0048895P.
XX		XX	97US-0048896P.
PA	(GENO-) GENOME THERAPEUTICS CORP.	PR	97US-0048897P.
XX		PR	97US-0048898P.
PI	Breton GL, Osborne M;	PR	97US-0048899P.
XX		PR	97US-0048900P.
DR	WPI; 2003-895346/82.	PR	97US-0048901P.
DR	N-PSDB; ACH95924.	PR	97US-0048915P.
XX		PR	97US-0048916P.
PT	New nucleic acid encoding a Klebsiella pneumoniae polypeptide, useful for	PR	97US-0048917P.
PT	preparing a vaccine composition against Klebsiella pneumoniae.	PR	97US-0048949P.
XX		PR	97US-0048962P.
PS	Disclosure; SEQ ID NO 8890; 932pp; English.	PR	97US-0048963P.
XX		PR	97US-0048964P.
CC	The invention describes a new isolated nucleic acid encoding a Klebsiella	PR	97US-0048970P.
CC	pneumoniae polypeptide. Also described are: a recombinant expression	PR	97US-0048971P.
CC	vector comprising the nucleic acid, operably linked to a transcription	PR	97US-0048972P.
CC	regulatory element; and a cell comprising the recombinant expression	PR	97US-0048974P.
CC	vector. The nucleic acid is useful for preparing a vaccine composition	PR	97US-0049019P.
CC	against Klebsiella pneumoniae. This is the amino acid sequence of a	PR	97US-0049020P.
CC	Klebsiella pneumoniae polypeptide of the invention	PR	97US-0049373P.
XX		PR	97US-0049374P.
SQ	Sequence 1107 AA;	PR	97US-0049375P.
		PR	97US-0057584P.
	Query Match 54.5%; Score 42.5; DB 7; Length 1107;	PR	97US-0057627P.
	Best Local Similarity 64.3%; Pred. No. 2.1e+02;	PR	97US-0057628P.
	Matches 9; Conservative 2; Mismatches 2; Indels 1; Gaps 1;	PR	97US-0057629P.
QY	1 RQR-LPKRMGGSYR 13	PR	97US-0057634P.
	: : :	PR	97US-0057635P.
Db	19 RQRFPDRLGGQYR 32	PR	97US-0057642P.
		PR	97US-0057643P.
		PR	97US-0057644P.
		PR	97US-0057645P.
		PR	97US-0057646P.
RESULT 11		PR	97US-0057647P.
AAW89049		PR	97US-0057648P.
ID	AAW89049 standard; protein; 30 AA.	PR	97US-0057649P.
XX		PR	97US-0057650P.
AC	AAW89049;	PR	97US-0057651P.
XX		PR	97US-0057654P.
DT	01-MAR-1999 (first entry)	PR	97US-0057661P.
XX		PR	97US-0057662P.
DE	Polypeptide fragment encoded by gene 183.	PR	97US-0057666P.
XX		PR	97US-0057667P.
KW	Human; secreted protein; fusion protein; gene therapy; protein therapy;	PR	97US-0057688P.
KW	diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia;	PR	97US-0057760P.
KW	developmental abnormality; foetal deficiency; blood; allergy; renal;	PR	97US-0057761P.
KW	immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma;	PR	97US-0057762P.
KW	inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS;	PR	97US-0057763P.
KW	cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus;	PR	97US-0057764P.
KW	osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;	PR	97US-0057765P.
KW	endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.	PR	97US-0057769P.
XX		PR	97US-0057770P.
OS	Homo sapiens.	PR	97US-0057771P.
XX		PR	97US-0057774P.
PN	WO9854963-A2.	PR	97US-0057775P.
XX		PR	97US-0057776P.
PD	10-DEC-1998.	PR	97US-0057777P.
XX		PR	97US-0057778P.
PF	04-JUN-1998; 98WO-US011422.	PR	97US-0070923P.
XX		XX	(HUMA-) HUMAN GENOME SCI INC.
XX		XX	Young P, Greene JM, Ferrie AM, Ruben SM, Rosen CA, Hu J;
PR	97US-0048875P.	PI	Olsen HS, Ebner R, Brewer LA, Moore PA, Shi Y, Florence C;
PR	97US-0048876P.	PI	Florence K, Lafleur DW, Ni J, Fan P, Wei Y, Fischer CL, Sopbet DR;
PR	97US-0048877P.	PI	Li Y, Zeng Z, Kyaw H, Yu G, Feng P, Dillon PJ, Endress GA;
PR	97US-0048878P.	PI	Carter KC;
PR	97US-0048880P.	XX	WPI; 1999-059865/05.
PR	97US-0048881P.	DR	N-PSDB; AAW84593.
PR	97US-0048882P.	DR	
PR	97US-0048883P.	DR	
PR	97US-0048884P.	DR	
PR	97US-0048885P.	DR	
PR	97US-0048892P.	DR	

XX New isolated human genes and the secreted polypeptides they encode -
PT useful for diagnosis and treatment of e.g. cancers, neurological
PT disorders, immune diseases, inflammation or blood disorders.
XX
PS Disclosure: Page 143; 772pp; English.
XX
CC The invention relates to nucleic acid sequences (AAV84411 to AAV84633)
CC encoding human secreted proteins (AAV88534 to AAV88756). The secreted
CC protein gene sequences are deposited with the ATCC under deposit numbers
CC ATCC 97979, 97974, 97975, 97976, 97977, 209007, 209008, 209009, 209010,
CC 209011, 209080, 209081, 209082, 209083, 209084, 209085, 209511. Host
CC cells comprising recombinant vectors containing the nucleic acid
CC sequences are used for the recombinant production of the secreted
CC proteins. The polynucleotide and amino acid sequences are useful for are
CC useful for preventing, treating or ameliorating medical conditions e.g.
CC by protein or gene therapy. Pathological conditions can be also diagnosed
CC by determining the amount of the new polypeptides in a sample or by
CC determining the presence of mutations in the new polynucleotides.
CC Specific uses are described for each of the polynucleotides, based on
CC which tissues they are most highly expressed in, and include developing
CC products for the diagnosis or treatment of cancer, neurodegenerative
CC disorders, developmental abnormalities and foetal deficiencies, blood
CC disorders, tumours, leukemias, diseases of the immune system, autoimmune
CC diseases, hepatic and renal disease, lymphomas, inflammation, allergies,
CC ischemic shock, Alzheimer's and cognitive disorders, schizophrenia,
CC restenosis, prostate diseases, obesity, disorders involving osteoclasts
CC such as osteoporosis, arthritis or malignancies, diseases of testes, lung
CC or thymus, digestive/endocrine disorders, infections and AIDS. The
CC polypeptides are also useful for identifying their binding partners. The
CC present sequence represents a polypeptide fragment encoded by a gene of
CC the invention (see descriptor line for gene number)
XX
SQ Sequence 30 AA;
Query Match 53.8%; Score 42; DB 2; Length 30;
Best Local Similarity 61.5%; Pred. No. 6.2;
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
QY 1 RQRLPRMGGSYR 13
Db |||||:
5 RQRRPRRGGTSR 17
RESULT 12
ABB51214
ID ABB51214 standard; protein; 30 AA.
XX
AC ABB51214;
XX
DT 07-FEB-2002 (first entry)
XX
DE Human secreted protein encoded by gene 183 SEQ ID NO:1167.
XX
DE Human; secreted protein; immunomodulatory; antisclerotic; anti-HIV;
KW dermatological; immunosuppressive; antiinflammatory; immunostimulant;
KW cytostatic; cardiant; vascular; anti-angiogenic; ophthalmological;
KW neuroprotective; nootropic; anticonvulsant; antialzheimers; vulnery;
KW antiparkinsonian; antimicrobial; gene therapy; vaccine; immune disorder;
KW multiple sclerosis; systemic lupus erythematosus; HIV infection; cancer;
KW human immunodeficiency virus; hyperproliferative disorder; wound healing;
KW Gaucher's disease; cardiovascular disease; Scimitar syndrome; chemotaxis;
KW Chaga's cardiomyopathy; coronary arteriosclerosis; angioecnic disorder;
KW corneal graft neovascularisation; diabetic retinopathy; regeneration;
KW neurological disorder; Huntington's chorea; Alzheimer's disease;
KW Parkinson's disease; infectious disease; chromosome 17.
XX
OS Homo sapiens.
XX
XX WO200162891-A2.
XX
XX 10-AUG-2001.
XX

PP 21-FEB-2001; 2001WO-US005614.
XX
PR 24-FEB-2000; 2000US-0184836P.
PR 29-MAR-2000; 2000US-0193170P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX NI J, Ebner R, Lafleur DW, Moore PA, Olsen HS, Rosen CA,
PI Ruben SM, Soppet DR, Young PE, Shi Y, Florence KA, Wei Y,
PI Florence C, Hu J, Li Y, Kyaw H, Fischer CL, Ferrie AM, Fan P,
PI Feng P, Endress GA, Dillon PJ, Carter KC, Brewer LA, Yu G, Zeng Z,
PI Greene JW;
XX
XX WPI; 2001-625724/72.
XX
XX Nucleic acids encoding 207 human secreted polypeptides, useful for
XX preventing, diagnosing and/or treating, e.g. cancers, Parkinson's disease
XX and diabetic retinopathy.
XX
XX Disclosure: Page 398; 1533pp; English.
XX
XX ABB50301 to ABB51287 and ABA83194 to ABA83441 represent human secreted
XX proteins (I) and polynucleotide (II) sequences. (I) and (II) have various
XX activities based on the tissues and cells the genes are expressed in.
XX Example of these activities include: immunomodulatory; antisclerotic;
XX dermatological; immunosuppressive; antiinflammatory; immunostimulant;
XX anti-HIV; cytostatic; cardiant; anti-angiogenic; ophthalmological;
XX neuroprotective; nootropic; anticonvulsant; antialzheimers; vascular;
XX antiparkinsonian; antimicrobial; and vulnery. (I) and (II) can be used
XX in gene therapy and vaccine production. (I) and (II) can be used in the
XX prevention, diagnosis and treatment of immune disorders (e.g. multiple
XX sclerosis, systemic lupus erythematosus and human immunodeficiency virus
XX (HIV) infections), hyperproliferative disorders (e.g. cancers and
XX Gaucher's disease), cardiovascular diseases (e.g. Scimitar syndrome,
XX Chaga's cardiomyopathy and coronary arteriosclerosis), angioecnic
XX disorders (e.g. corneal graft neovascularisation and diabetic
XX retinopathy), neurological disorders (e.g. Huntington's chorea,
XX Alzheimer's disease and Parkinson's disease), infectious diseases and/or
XX for promoting wound healing, regeneration and/or chemotaxis. ABA83195 to
XX ABA83193 and ABB50300 represent sequences used in the exemplification of
XX the present invention
XX
SQ Sequence 30 AA;
Query Match 53.8%; Score 42; DB 4; Length 30;
Best Local Similarity 61.5%; Pred. No. 6.2;
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
QY 1 RQRLPRMGGSYR 13
Db |||||:
5 RQRRPRRGGTSR 17
RESULT 13
ABO45471
ID ABO45471 standard; protein; 30 AA.
XX
AC ABO45471;
XX
DT 03-OCT-2003 (first entry)
XX
DE Novel human secreted protein #183 fragment #3.
XX
XX Human; gene therapy; autoimmune disorder; multiple sclerosis; cancer;
KW systemic lupus erythematosus; haematopoietic cell disorder; allergy;
KW agammaglobulinaemia; ataxia telangiectasia; blood coagulation disorder;
KW afibrinogenemia; thrombocytopenia; graft-versus-host disease; arthritis;
KW inflammatory condition; ischaemia-reperfusion injury; infectious disease;
KW hyperproliferative disorder; purpura; viral infection; regeneration;
KW bacterial infection; ulcer; Alzheimer's disease.
XX
OS Homo sapiens.
XX

XX 23-MAR-2000; 2000US-0191637P.
 PR 11-JUL-2000; 2000US-00614150.
 XX (PEKE) PE CORP NY.
 XX Venter JC, Adams M, Li PWD, Myers EW,
 PI WFI; 2001-656860/75.
 XX DR N-PSDB; ABL12653.
 DR
 XX New isolated nucleic acid detection reagent for detecting 1000 or more
 PT genes from Drosophila and for elucidating cell signaling and cell-cell
 PT interactions.
 PT
 XX Disclosure; SEQ ID NO 32442; 21pp + Sequence Listing; English.
 PS
 XX The invention relates to an isolated nucleic acid detection reagent
 CC capable of detecting 1000 or more genes from Drosophila. The invention is
 CC useful in developmental biology and in elucidating cell signalling and
 CC cell-cell interactions in higher eukaryotes for the development of
 CC insecticides, therapeutics and pharmaceutical drugs. The invention
 CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
 CC sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-
 CC ABB72072). The sequence data for this patent did not form part of the
 CC printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 339 AA;

Query Match 53.8%; Score 42; DB 4; Length 339;
 Best Local Similarity 70.0%; Pred. No. 75;
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 5 PKRMGGSYRC 14
 |||:|
 Db 208 PKRVPGPYRC 217

Search completed: November 18, 2005, 00:27:53
 Job time : 81 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model.

Run on: November 17, 2005, 22:32:53, Search time 23 Seconds
(without alignments)
58.567 Million cell updates/sec

Title: US-09-745-008-14

Perfect score: 78

Sequence: 1 RQRLPRMGGSYRC 14

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 79:*

1: P1r1:*

2: P1r2:*

3: P1r3:*

4: P1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	78	100.0	1162	2 JH0557	exo-alpha-sialidas
2	41	52.6	83	2 AE1851	hypothetical prote
3	41	52.6	564	2 H75403	glycosyl hydrolase
4	40.5	51.9	235	2 JU0029	tumor necrosis fac
5	40	51.3	230	2 G65067	hypothetical prote
6	40	51.3	230	2 B85937	hypothetical prote
7	40	51.3	230	2 G91091	hypothetical prote
8	40	51.3	261	2 JQ0137	hypothetical 30.1K
9	40	51.3	314	2 F75504	probable pilin, ty
10	40	51.3	428	2 H86890	hypothetical prote
11	40	51.3	538	2 T51756	NAD+ synthase (glu
12	40	51.3	1559	2 T07757	probable DNA (cyto
13	39	50.0	298	2 B71013	hypothetical prote
14	39	50.0	332	2 G81395	probable ATP /GTP
15	39	50.0	372	2 C90498	carnitine dehydrat
16	39	50.0	395	2 A92115	conserved hypotet
17	39	50.0	395	2 AH3071	probable histidine
18	39	50.0	472	2 T06637	vitroplasmin - cau
19	39	50.0	520	2 S11217	protein unc-73b li
20	39	50.0	1638	2 D87749	Xin protein, stage
21	39	50.0	1677	2 T14267	guanine nucleotide
22	39	50.0	2488	2 T42739	hypothetical prote
23	38	48.7	210	2 S28673	hypothetical prote
24	38	48.7	356	2 F95954	probable dTPgluco
25	38	48.7	422	2 T21820	hypothetical prote
26	38	48.7	553	2 C13741	glycerol kinase -
27	38	48.7	781	2 C69452	signal-transducing
28	38	48.7	876	2 T19246	hypothetical prote
29	38	48.7	1403	2 S24548	homeotic protein p

RESULT 1

JH0557

exo-alpha-sialidase (EC 3.2.1.18) - Trypanosoma cruzi

N:Alternate names: neuraminidase

C:Species: Trypanosoma cruzi

C>Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004

C:Accession: JH0557

R: Pereira, M.E.A.; Mejia, J.S.; Ortega-Barria, E.; Matzilevich, D.; Prioli, R.P.

J: Exp. Med. 174, 179-191, 1991

A: Title: The Trypanosoma cruzi neuraminidase contains sequences similar to bacterial ne

A: Reference number: JH0557; MUID:91277609; PMID:1711561

A: Accession: JH0557

A: Molecule type: DNA

A: Residues: 1-1162 <PER>

A: Cross-references: UNIPROT:P23253; GB:M61732; NID:gl62302; PID:gl62303

A: Note: The authors translated the codon TCT for residue 45 as Cys

C: Comment: This protein plays a role in parasite-host cell interaction.

C: Superfamily: trypanostigote-specific surface antigen

C: Keywords: glycoprotein; glycosidase; hydrolase

F:394/Binding site: carbohydrate (Aan) (covalent) #status predicted

Query Match 100.0%; Score 78; DB 2; Length 1162;

Best Local Similarity 100.0%; Pred. No. 2.4e-05;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RQRLPRMGGSYRC 14

DB 379 RQRLPRMGGSYRC 392

RESULT 2

AE1851

hypothetical protein asr0358 [imported] - Nostoc sp. (strain PCC 7120)

C: Species: Nostoc sp. PCC 7120

A: Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120

C: Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 03-Jul-2004

C: Accession: AE1851

R: Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi;

Nakazaki, N.; Shimpou, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, I

DNA Res. 8, 205-213, 2001

A: Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium An

A: Reference number: AB1807; MUID:21595285; PMID:11759840

A: Accession: AE1851

A: Status: Preliminary

A: Molecule type: DNA

A: Residues: 1-83 <KUR>

A: Cross-references: UNIPROT:Q8YZU7; GB:BA000019; PIDN:BA072316.1; PID:gl7129703; GSPDB:C

A: Experimental source: strain PCC 7120

C: Genetics:

A: Gene: asr0358

Query Match 52.6%; Score 41; DB 2; Length 83;

Best Local Similarity 38.5%; Pred. No. 5.8;
Matches 5; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

QY 2 QRLPKRMGGSYRC 14
Db 46 RNIAKUGGNPRC 58

RESULT 3
H75403
glycosyl hydrolase, family 13 - Deinococcus radiodurans (strain R1)
C/Species: Deinococcus radiodurans
C/Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C/Accession: H75403
R/White, O.; Eise, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A/Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A/Reference number: A75250; MUID:20036896; PMID:10567266
A/Accession: H75403
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-564 <WHI>
A/Cross-references: UNIPROT:Q9RUK9; GB:AE001983; GB:AE000513; NID:G6459123; PIDN:AAF1094
A/Experimental source: strain R1
C/Genetics:
A/Map position: 1
C/Superfamily: alpha-glucosidase; alpha-amylase core homology

Query Match 52.6%; Score 41; DB 2; Length 564;
Best Local Similarity 61.5%; Pred. No. 34;
Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 RQRLPKRMGGSYR 13
Db 487 RQEPALVGGSYR 499

RESULT 4
JU0029
tumor necrosis factor alpha precursor - rat
N/Alternate names: cachectin; TNF alpha
C/Species: Rattus norvegicus (Norway rat)
C/Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 09-Jul-2004
C/Accession: JU0029; JN0868; S21674
R/Shirai, T.; Shimizu, N.; Horiguchi, S.; Ito, H.
Agric. Biol. Chem. 53, 1733-1736, 1989
A/Title: Cloning and expression in Escherichia coli of the gene for rat tumor necrosis f
A/Reference number: JU0029
A/Accession: JU0029
A/Molecule type: DNA
A/Residues: 1-235 <SHI>
A/Cross-references: UNIPROT:P16599
R/Kwon, J.; Chung, I.Y.; Benveniste, E.N.
Gene 132, 227-236, 1993
A/Title: Cloning and sequence analysis of the rat tumor necrosis factor-encoding genes.
A/Reference number: JN0868; MUID:94040766; PMID:8224868
A/Accession: JN0868
A/Molecule type: DNA
A/Residues: 1-235 <KWO>
A/Cross-references: GB:L00981; NID:G205253; PIDN:AAA16275.1; PID:G205254
R/Batler, H.C.; Graw, M.; Gausling, R.; Pavlovic, M.; Decker, K.
Biol. Chem. Hoppe-Seyler 373, 271-281, 1992
A/Title: Rat tumor necrosis factor-alpha. Transcription in rat Kupffer cells and in vitr
A/Reference number: S21674; MUID:92329007; PMID:1627266
A/Accession: S21674
A/Molecule type: mRNA
A/Residues: 1-38, 'P', 40-162, 'T', 164-201, 'S', 203-235 <EST>
A/Cross-references: GB:X66539; GB:S40199; NID:G395369; PIDN:CAA47146.1; PID:G395370
C/Comment: Tumor necrosis factor is secreted by macrophages in response to endotoxin and
C/Genetics:

A/Gene: TNF-alpha
A/Introns: 62/3; 81/1; 97/1
C/Superfamily: tumor necrosis factor
C/Keywords: cytokine; cytotoxin; glycoprotein; lipoprotein; lymphokine; macrophage; mem
F/80-235/Product: tumor necrosis factor #status predicted <MAI>
F/19/20/Binding site: myristate (Lys) (covalent) #status predicted
F/84/Binding site: carbohydrate (Ser) (covalent) #status predicted
F/86/Binding site: carbohydrate (Asn) (covalent) #status predicted
F/148-179/Disulfide bonds: #status predicted

Query Match 51.9%; Score 40.5; DB 2; Length 235;
Best Local Similarity 56.2%; Pred. No. 18;
Matches 9; Conservative 2; Mismatches 2; Indels 3; Gaps 1;

QY 2 QRLPKRMGG--SYRC 14
Db 15 EALPKRMGGGLQNSRC 30

RESULT 5
G65067
hypothetical protein b2846 - Escherichia coli (strain K-12)
C/Species: Escherichia coli
C/Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 01-Mar-2002
C/Accession: G65067
R/Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; C
A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A/Title: The complete genome sequence of Escherichia coli K-12.
A/Reference number: A64720; MUID:97426617; PMID:9278503
A/Accession: G65067
A/Status: preliminary; nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA
A/Residues: 1-230 <BLAT>
A/Cross-references: GB:AB000368; GB:U00096; NID:G3267165; PIDN:AACT5885.1; PID:G1789912;
A/Experimental source: strain K-12, substrain MGL655

Query Match 51.3%; Score 40; DB 2; Length 230;
Best Local Similarity 70.0%; Pred. No. 22;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 RQRLPKRMGG 10
Db 207 KQRIKRMGG 216

RESULT 6
B85937
hypothetical protein yqeh [imported] - Escherichia coli (strain O157:H7, substrain EDL9;
C/Species: Escherichia coli
C/Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C/Accession: B85937
R/Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhe
iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, S.; Potamousis, K.; Apodaca,
Nature 409, 529-533, 2001
A/Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A/Reference number: A85480; MUID:21074935; PMID:11206551
A/Accession: B85937
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-230 <STO>
A/Cross-references: UNIPROT:Q8X615; GB:AE005174; NID:G12517338; PIDN:AAGS7958.1; GSPDB:1;
A/Experimental source: strain O157:H7, substrain EDL933
C/Genetics:
A/Gene: yqeh

Query Match 51.3%; Score 40; DB 2; Length 230;
Best Local Similarity 70.0%; Pred. No. 22;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 RQRLPKRMGG 10
Db 207 KQRIKRMGG 216

RESULT 7
G91091

hypothetical protein Ecs3703 [imported] - Escherichia coli (strain O157:H7, substrain R1)
C:Species: Escherichia coli
C:Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
C:Accession: G91091
R:Hayaashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.-G.;
Gawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genome
A:Reference number: A99629; MUID:21156231; PMID:11258796
A:Accession: G91091
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-230 <HAY>
A:Cross-references: UNIPROT:Q8XG15; GB:BA000007; PIDN:BA037126.1; PID:g133631175; GSPDB:G
A:Experimental source: strain O157:H7, substrain R1MD 0509952
C:Genetics:
A:Gene: Ecs3703

Query Match 51.3%; Score 40; DB 2; Length 230;
Best Local Similarity 70.0%; Pred. No. 22;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 RORLPKRMGG 10
|||:|||||
DB 207 KORIEKRMGG 216

RESULT 8

JQ0137
hypothetical 30.1k protein - Pseudomonas aeruginosa
C:Species: Pseudomonas aeruginosa
C:Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 07-Jun-1996
C:Accession: JQ0137
R:Kato, J.; Chu, L.; Kitano, K.; DeVault, J.D.; Kimbara, K.; Chakrabarty, A.M.; Misra, T.
Gene 84, 31-38, 1989
A:Title: Nucleotide sequence of a regulatory region controlling alginate synthesis in P
A:Reference number: JQ0137; MUID:90108714; PMID:2514124
A:Accession: JQ0137
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-261 <XAT>
A:Note: 3-Met could also be the initiator
C:Genetics:
A:Start codon: GTG

Query Match 51.3%; Score 40; DB 2; Length 261;
Best Local Similarity 57.1%; Pred. No. 25;
Matches 8; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 RORLPKRMGGSYRC 14
|||:|||||
DB 31 RORLRRWSGRRRC 44

RESULT 9

P75504
probable pilin, type IV - Deinococcus radiodurans (strain R1)
C:Species: Deinococcus radiodurans
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C:Accession: P75504
R:White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
M.J. Shen, M.; Vanathavan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zaleski, C.; Ma
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A:Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A:Reference number: A75250; MUID:20036896; PMID:10567266
A:Accession: P75504
A:Status: preliminary
A:Molecule type: DNA

QY 5 PKRMGGSYRC 14
|||:|||||
DB 233 PRLGGSSRC 242

A:Residues: 1-314 <WHI>
A:Cross-references: UNIPROT:Q9RWM7; GB:AE001913; GB:AE000513; MID:96458240; PIDN:AAF101
A:Experimental source: strain R1
C:Genetics:
A:Gene: DR0548
A:Map position: 1

Query Match 51.3%; Score 40; DB 2; Length 314;
Best Local Similarity 72.7%; Pred. No. 30;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 RORLPKRMGG 11
|||:|||||
DB 26 RORGPORQGS 36

RESULT 10

H86890
hypothetical protein yvjB [imported] - Lactococcus lactis subsp. lactis (strain IL1403)
C:Species: Lactococcus lactis subsp. lactis
C:Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 09-Jul-2004
C:Accession: H86890
R:Botolin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarme, K.; Weissenbach, J.; Ehrh
Genome Res. 11, 731-753, 2001
A:Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis s
A:Reference number: A86625; MUID:21235186; PMID:11337471
A:Accession: H86890
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-428 <STO>
A:Cross-references: UNIPROT:Q9CDT3; GB:AE005176; PID:g12725185; PIDN:AAK06226.1; GSPDB:
A:Experimental source: strain IL1403
C:Genetics:
A:Gene: yvjB

Query Match 51.3%; Score 40; DB 2; Length 428;
Best Local Similarity 77.8%; Pred. No. 39;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 PKRMGGSYRC 13
|||:|||||
DB 280 PKMGDSYRC 288

RESULT 11

T51756
NAD+ synthase (glutamine-hydrolyzing) (EC 6.3.5.1) [imported] - Streptomyces coelicolor
C:Species: Streptomyces coelicolor
C:Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 09-Jul-2004
C:Accession: T51756
R:Fink, D.; Falke, D.; Wohlleben, W.; Engels, A.
Microbiology 145, 2313-2322, 1999
A:Title: Nitrogen metabolism in Streptomyces coelicolor A3(2): modification of glutamin
A:Reference number: Z25448
A:Accession: T51756
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-538 <FIN>
A:Cross-references: UNIPROT:Q9ZAV9; EMBL:Y17736; PIDN:CAB38325.1
A:Experimental source: strain A3(2)
C:Genetics:
A:Gene: nade
C:Superfamily: Rhodobacter capsulatus NH3-dependent NAD+ synthase
C:Keywords: ligase

Query Match 51.3%; Score 40; DB 2; Length 538;
Best Local Similarity 70.0%; Pred. No. 49;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 5 PKRMGGSYRC 14
|||:|||||
DB 233 PRLGGSSRC 242

RESULT 12

T07757
Probable DNA (cytosine-5-)-methyltransferase (EC 2.1.1.37) - tomato
C/Species: Lycopersicon esculentum (tomato)
C/Date: 14-May-1999 #sequence_revision 14-May-1999 #text_change 09-Jul-2004
C/Accession: T07757
R/Cella, R.
submitted to the EMBL Data Library, October 1997
A/Reference number: Z16119
A/Accession: T07757
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-1559 <CEL>
A/Cross-references: UNIPROT:O49889; EMBL:AJ002140; NID:e1250983; PIDN:CAA05207.1; PID:el
A/Experimental source: cultivar Meraviglia; apical meristems
C/Genetics:
A/Gene: sMET
C/Keywords: methyltransferase; S-adenosylmethionine

Query Match 51.3%; Score 40; DB 2; Length 1559;
Best Local Similarity 58.3%; Pred. No. 1.3e+02;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 2 QRLPKRMGGSYR 13

|:|:|:|:|:|

Db 1423 QRIPKPGADWR 1434

RESULT 13

B71013
hypothetical protein PH1400 - Pyrococcus horikoshii
C/Species: Pyrococcus horikoshii
C/Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 09-Jul-2004
C/Accession: B71013
R/Kawarabayashi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Sekin
M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguchi
DNA Res. 5, 55-76, 1998
A/Title: Complete sequence and gene organization of the genome of a hyper-thermophilic a
A/Reference number: A71000; MUID:98344137; PMID:9679194
A/Accession: B71013
A/Status: preliminary; nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA
A/Residues: 1-298 <KAW>
A/Cross-references: UNIPROT:O50108; GB:AP000006; NID:G2236133; PIDN:BAA30506.1; PID:d103
A/Experimental source: strain OT3
A/Note: this accession replaces an interim accession for a sequence replaced by GenBank
C/Genetics:
A/Gene: PH1400

Query Match 50.0%; Score 39; DB 2; Length 298;

Best Local Similarity 63.6%; Pred. No. 42;

Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 3 RLPKRMGGSYR 13

|:|:|:|:|:|

Db 51 RLKRLGGIYK 61

RESULT 14

G81395
Probable ATP /GTP binding protein Cj0500 [imported] - Campylobacter jejuni (strain NCTC
C/Species: Campylobacter jejuni
C/Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
C/Accession: G81395
R/Parkhill, J.; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chilling
C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; Barrel
Nature 403, 665-669, 2000
A/Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hyp
A/Reference number: A81250; MUID:20150912; PMID:10688204
A/Accession: G81395
A/Status: preliminary
A/Molecule type: DNA

A/Residues: 1-332 <PAR>

A/Cross-references: UNIPROT:Q9PI09; GB:AL139075; GB:AL111168; NID:G6967817; PIDN:CAB751;
A/Experimental source: serotype O2, strain NCTC 11168

C/Genetics:

A/Gene: Cj0500

Query Match 50.0%; Score 39; DB 2; Length 332;
Best Local Similarity 61.5%; Pred. No. 46;
Matches 8; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2 QRLPKRMGGSYR 14

|:|:|:|:|:|

Db 57 QALAKAMGASYIC 69

RESULT 15

C90498
carnitine dehydratase, probable [imported] - Sulfolobus solfataricus
C/Species: Sulfolobus solfataricus
C/Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004
C/Accession: C90498
R/She, O.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan-
Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, I.
arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.
submitted to GenBank, April 2001
A/Description: Sulfolobus solfataricus complete genome.
A/Reference number: A99139
A/Accession: C90498
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-372 <KUR>
A/Cross-references: UNIPROT:Q97U79; GB:AE006641; NID:g13816568; PIDN:AAK43242.1; GSPDB:
C/Genetics:
A/Gene: S803144
C/Superfamily: Mycobacterium tuberculosis hypothetical protein RV3272

Query Match 50.0%; Score 39; DB 2; Length 372;

Best Local Similarity 54.5%; Pred. No. 52;

Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 3 RLPKRMGGSYR 13

|:|:|:|:|:|

Db 209 KVPKRMGSAHR 219

Search completed: November 18, 2005, 00:29:46

Job time : 27 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 17, 2005, 22:29:58 ; Search time 79 Seconds
(without alignments)
90.748 Million cell updates/sec

Title: US-09-745-008-14

Perfect score: 78

Sequence: 1 RQRLPRMGGSYRC 14

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt 03.1*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	78	100.0	1162	1 TCNA_TRYCR	P23253 trypanosoma
2	47	60.3	487	2 Q6LG50	Q61950 photobacter
3	47	60.3	487	2 Q7MB24	Q7mb24 vibrio vuln
4	47	60.3	487	2 Q8D557	Q8d557 vibrio vuln
5	47	60.3	488	2 Q87FH4	Q87fh4 vibrio para
6	44	56.4	244	2 Q8JXU8	Q8jku8 heliothis z
7	44	56.4	823	2 Q7PQ04	Q7psq4 anopheles g
8	43	55.1	224	2 Q6ZQ04	Q6zon4 oryza sativ
9	42	53.8	107	2 Q68807	Q68807 synchococc
10	42	53.8	339	2 Q9VUB3	Q9vub3 drosophila
11	42	53.8	474	2 Q89V78	Q89v78 bradyrhizob
12	42	53.8	722	2 Q6GNB3	Q6gnb3 xenopus lae
13	42	53.8	1169	1 IF2_PROMP	Q7uzs9 prochloroco
14	41	52.6	83	2 Q8YZ07	Q8yzu7 anabaena sp
15	41	52.6	384	2 Q7UES8	Q7ues8 rhodospirell
16	41	52.6	564	2 Q9RUK9	Q9ruk9 deinococcus
17	41	52.6	694	2 Q63J17	Q63j17 burkholderi
18	41	52.6	1055	2 Q6M221	Q6mg21 rattus norv
19	40.5	51.9	235	1 TNFA_RAT	P16599 rattus norv
20	40.5	51.9	748	2 Q8LQH6	Q8lqh6 oryza sativ
21	40	51.3	150	2 Q82J86	Q82j86 streptomyc
22	40	51.3	151	2 Q9K4D3	Q9k4d3 streptomyc
23	40	51.3	181	2 Q6H705	Q6h705 oryza sativ
24	40	51.3	220	1 Q6EH_ECOLI	Q46941 escherichia
25	40	51.3	230	2 Q8X615	Q8x615 escherichia
26	40	51.3	314	2 Q9RWM7	Q9rwm7 deinococcus
27	40	51.3	384	2 Q657J9	Q657j9 oryza sativ
28	40	51.3	428	1 YL28_LACLA	Q9cdt3 lactococcus
29	40	51.3	507	2 Q8KW84	Q8kw84 ruegeria sp
30	40	51.3	533	2 Q6ZIE6	Q6zie6 oryza sativ
31	40	51.3	538	2 Q9Z4V9	Q9z4v9 streptomyc

32	40	51.3	559	2	Q969Y0	Q969y0 homo sapien
33	40	51.3	885	2	Q8HYV1	Q8hyv1 sus scrofa
34	40	51.3	886	2	Q8HYV2	Q8hyv2 sus scrofa
35	40	51.3	953	1	MDG1_HUMAN	Q8nfp4 homo sapien
36	40	51.3	1556	2	Q9MB97	Q9mb97 nicotiana t
37	40	51.3	1559	2	Q49889	Q49889 lycopersico
38	40	51.3	1955	2	Q8W078	Q8w078 oryza sativ
39	39.5	50.6	619	2	Q8BWQ5	Q8bwq5 mus musculus
40	39	50.0	61	2	Q83177	Q83177 cauliflower
41	39	50.0	203	2	Q8N9P6	Q8n9p6 homo sapien
42	39	50.0	277	2	Q7X801	Q7x801 oryza sativ
43	39	50.0	298	2	Q50108	Q50108 pyrococcus
44	39	50.0	304	1	K2S3_HUMAN	Q14952 homo sapien
45	39	50.0	311	1	STCC_EMENI	Q00668 emericella

ALIGNMENTS

RESULT 1

TCNA_TRYCR	ID	TCNA_TRYCR	STANDARD	PRT	1162 AA
AC	P23253				
DT	01-NOV-1991	(Rel. 20, Created)			
DT	01-NOV-1991	(Rel. 20, Last sequence update)			
DT	25-OCT-2004	(Rel. 45, Last annotation update)			
DE	Slalidase [EC 3.2.1.18] (Neuraminidase) (NA) (Major surface antigen).				
GN	Names=TCNA;				
OS	Trypanosoma cruzi.				
OC	Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.				
OX	NCBI_TaxID=5693;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=Silvio X-10/4;				
RX	MEDLINE=91277609; PubMed=1711561;				
RA	Pereira M.E.A., Mejia J.S., Ortega-Barria E., Matzilevich D., Prioli R.P.;				
RT	"The Trypanosoma cruzi neuraminidase contains sequences similar to bacterial neuraminidases, YWTD repeats of the low density lipoprotein receptor, and type III modules of fibronectin."				
RL	J. Exp. Med. 174:179-191(1991).				
RN	[2]				
RP	SUBCELLULAR LOCATION.				
RX	MEDLINE=91376547; PubMed=1896773;				
RA	Prioli R.P., Mejia J.S., Aji T., Aikawa M., Pereira M.E.A.;				
RT	"Trypanosoma cruzi: localization of neuraminidase on the surface of trypanosomatids."				
RL	Trop. Med. Parasitol. 42:146-150(1991).				
CC	-I- FUNCTION: Developmentally regulated neuraminidase implicated in parasite invasion of cells.				
CC	-I- CATALYTIC ACTIVITY: Hydrolysis of alpha-(2-3)-, alpha-(2-6)-, alpha-(2-8)-glycosidic linkages of terminal sialic residues in oligosaccharides, glycoproteins, glycolipids, colominic acid and synthetic substrates.				
CC	-I- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor (potential).				
CC	-I- DEVELOPMENTAL STAGE: Maximal activity in trypanosomatids, minimum in epimastigotes and not detectable in amastigotes.				
CC	-I- MISCELLANEOUS: The variable lengths of the long tandem repeat domain could account in part for the polymorphism of the TCNA protein.				
CC	-I- SIMILARITY: Belongs to the glycosyl hydrolase 33 family.				
CC	-I- SIMILARITY: Contains 3 BNR repeats.				
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).				
CC	EMBL; M61732; AAA30255.1; -				

```

DR PIR: JH0557; JH0557.
DR HSP: Q26966; 1MR5.
DR InterPro; IPR009985; ConA_like_lect_gly.
DR InterPro; IPR002860; Glyco_hydro_BNR.
DR InterPro; IPR011040; Sialidase.
DR InterPro; IPR008377; Sialidase_trypan.
DR Pfam; PF02012; BNR. 2.
DR PRINTS; PR01803; TCSIALIDASE.
DR Glycoprotein; Glycosidase; GPI-anchor; Hydrolase; Phosphorylation;
KW Repeat.
FT DOMAIN 1 457 Cys-rich.
FT REPEAT 23 34 BNR 1.
FT REPEAT 163 174 BNR 2.
FT REPEAT 209 220 BNR 3.
FT DOMAIN 458 588 Fibronectin type-III.
FT DOMAIN 589 1120 44 X 12 AA tandem repeats, LTR domain.
FT CARBOHYD 342 342 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 394 394 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 1125 1125 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 1162 AA; 120032 MW; 07049221897C6A40 CRC64;

Query Match 100.0%; Score 78; DB 1; Length 1162;
Best Local Similarity 100.0%; Pred. No. 3.6e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RQLPKRMGGSYR 14
Db |||||:|||||
379 RQLPKRMGGSYR 392

RESULT 2
Q6LG50 PRELIMINARY; PRT; 487 AA.
AC Q6LG50;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Putative mannose oxidoreductase.
GN Name=Y2903; OrderedLocNames=PPRBI180;
OS Photobacterium profundum (Photobacterium sp. (strain SS9)).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Photobacterium.
OX NCBI_TaxID=74109;
RN [1]
RP SEQUENCE FROM N.A.
RA Vezzi A., Campanaro S., D'Angelo M., Simonato F., Vitulo N., Lauro F.,
RA Cestaro A., Malacrida G., Simonati B., Cannata N., Bartlett D.,
RA Valle G.;
RT "Genome analysis of Photobacterium profundum reveals the complexity of
RT high pressure adaptations.";
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; CR378690; CAG23730.1; -.
DR GO; GO:0003824; F:catalytic activity; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR008927; 6GDGH C-like.
DR InterPro; IPR000669; Mannitol_dh.
DR Pfam; PF01232; Mannitol_dh; 1.
DR PRINTS; PR00084; MTLDDHGNASE.
DR PROSITE; PS00974; MANNITOL_DHGENASE; 1.
KW Complete proteome.
SQ SEQUENCE 487 AA; 53733 MW; 35525999038BB279 CRC64;

Query Match 60.3%; Score 47; DB 2; Length 487;
Best Local Similarity 66.7%; Pred. No. 7.3;
Matches 8; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 2 QRLPKRMGGSYR 13
Db |||||:|||||
376 QKIPQRMGGSLR 387

RESULT 3
Q7MB24 PRELIMINARY; PRT; 487 AA.
AC Q7MB24;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Mannonate oxidoreductase.
GN OrderedLocNames=VVA1593;
OS Vibrio vulnificus (strain YJ016).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrio.
OX NCBI_TaxID=196600;
RN [1]
RP SEQUENCE FROM N.A.
RA Chen C.-Y., Wu K.-M., Chang Y.-C., Chang C.-H., Tsai H.-C.,
RA Liao T.-L., Liu Y.-M., Chen H.-J., Shen A.B.-T., Li J.-C., Su T.-L.,
RA Shao C.-P., Lee C.-T., Hor L.-I., Tsai S.-F.;
RT "Comparative genome analysis of Vibrio vulnificus, a marine
RT pathogen.";
RL Genome Res. 13:2577-2587(2003).
DR EMBL; AF005350; BAC97619.1; -.
DR HSP; O08355; 1LJ8.
DR GO; GO:0003824; F:catalytic activity; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR008927; 6GDGH C-like.
DR InterPro; IPR000669; Mannitol_dh.
DR Pfam; PF01232; Mannitol_dh; 1.
DR PRINTS; PR00084; MTLDDHGNASE.
DR PROSITE; PS00974; MANNITOL_DHGENASE; 1.
KW Complete proteome.
SQ SEQUENCE 487 AA; 53290 MW; 570C961191EB96CE CRC64;

Query Match 60.3%; Score 47; DB 2; Length 487;
Best Local Similarity 66.7%; Pred. No. 7.3;
Matches 8; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 2 QRLPKRMGGSYR 13
Db |||||:|||||
376 QKIPQRMGGSLR 387

RESULT 4
Q8D557 PRELIMINARY; PRT; 487 AA.
AC Q8D557;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Mannitol-1-phosphate/altronate dehydrogenase.
GN OrderedLocNames=VW1069;
OS Vibrio vulnificus.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrio.
OX NCBI_TaxID=672;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CMCP6;
RA Rhee J.H., Kim S.Y., Chung S.S., Kim J.J., Moon Y.H., Jeong H.,
RA Choy H.E.;
RT "Complete genome sequence of Vibrio vulnificus CMCP6.";
RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AS016811; AAC07976.1; -.
DR HSP; O08355; 1LJ8.
DR GO; GO:0003824; F:catalytic activity; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR008927; 6GDGH C-like.
DR InterPro; IPR000669; Mannitol_dh.
DR Pfam; PF01232; Mannitol_dh; 1.
DR PRINTS; PR00084; MTLDDHGNASE.
DR PROSITE; PS00974; MANNITOL_DHGENASE; 1.
KW Complete proteome.
SQ SEQUENCE 487 AA; 53408 MW; 28786B2A15172F7D CRC64;

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Query Match      60.3%; Score 47; DB 2; Length 487;
Best Local Similarity 66.7%; Pred. No. 7.3;
Matches 8; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 2 QRLPKRMGGSYR 13
Db 376 QKIPQRMGGSLR 387

RESULT 5
Q87FH4
ID Q87FH4 PRELIMINARY; PRT; 488 AA.
AC Q87FH4;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Mannonate oxidoreductase.
GN OrderedLocusNames=VPAL1705;
OS Vibrio parahaemolyticus.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrrio.
OX NCBI_TaxID=670;
RN [1]
RC SEQUENCE FROM N.A.
RX STRAIN=RIND 2210633 / Serotype O3:K6;
RX MEDLINE=22508454; PubMed=12620739; DOI=10.1016/S0140-6736(03)12659-1;
RA Makino K., Oshima K., Kurokawa K., Yokoyama K., Uda T., Tagomori K.,
RA Iijima Y., Najima M., Nakano M., Yamashita A., Kubota Y., Kimura S.,
RA Yaenunaga T., Honda T., Shinagawa H., Hattori M., Iida T.;
RT "Genome sequence of Vibrio parahaemolyticus: a pathogenic mechanism
RT distinct from that of V. cholerae."
RT Lancet 361:743-749(2003).
DR EMBL; AF005089; BAC63048.1; -.
DR HSSP; Q08355; 1LJ8.
DR GO; GO:0003824; F:catalytic activity; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR008927; 6GDH_C-like.
DR InterPro; IPR000869; Mannitol dh.
DR Pfam; PF01232; Mannitol dh; 1.
DR PRINTS; PR00084; MTLIDHGNASE.
DR PROSITE; PS00974; MANNITOL_DHGENASE; 1.
KW Complete proteome.
SQ SEQUENCE 488 AA; 53509 MW; 700ED77B6BD56F4 CRC64;

Query Match      60.3%; Score 47; DB 2; Length 488;
Best Local Similarity 66.7%; Pred. No. 7.4;
Matches 8; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 2 QRLPKRMGGSYR 13
Db 376 QKIPQRMGGSLR 387

RESULT 6
Q8JKB8
ID Q8JKB8 PRELIMINARY; PRT; 244 AA.
AC Q8JKB8;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Orf13.
GN Name=orf13;
OS Heliothis zea virus 1.
OC Viruses; dsDNA viruses, no RNA stage; unclassified dsDNA viruses.
OX NCBI_TaxID=29250;
RN [1]
RC SEQUENCE FROM N.A.
RX MEDLINE=22174892; PubMed=12186886;
RX DOI=10.1128/JVI.76.18.9024-9034.2002;
RA Cheng C.H., Liu S.M., Chow T.Y., Hsiao Y.Y., Wang D.P., Huang J.J.,
RA Chen H.H.;
RT "Analysis of the complete genome sequence of the Hz-1 virus suggests
RT that it is related to members of the Baculoviridae."

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RL J. Virol. 76:9034-9034 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RA Cheng C.H., Liu H.M., Hsiao Y.Y., Chow T.Y., Chen H.H.;
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Chao Y.;
RL Submitted (NOV-1993) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA Chen H.H., Yeh W.B., Tso D.J.;
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RA Cheng C.H., Hsiao Y.Y., Liu S.M., Chow T.Y., Chen H.H.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF451898; AAN04308.1; -.
SQ SEQUENCE 244 AA; 28641 MW; 3DA50433EE14D855 CRC64;

Query Match      56.4%; Score 44; DB 2; Length 244;
Best Local Similarity 53.8%; Pred. No. 13;
Matches 7; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 1 RQRLPKRMGGSYR 13
Db 14 KERTPKLEGTYR 26

RESULT 7
Q7PSQ4
ID Q7PSQ4 PRELIMINARY; PRT; 823 AA.
AC Q7PSQ4;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE ENSANGP0000017954 (Fragment).
GN Name=ENSANGG0000015465;
OS Anopheles gambiae str. PEST.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae; Anopheles.
OX NCBI_TaxID=180454;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PEST;
RA Anopheles Genome Sequencing Consortium;
RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AAB01008816; EAA05197.2; -.
DR HSSP; P35555; 1EMN.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR InterPro; IPR000152; Abx_hydroxyl_S.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR006209; EGF_Like.
DR Pfam; PF00008; EGF_1.
DR Pfam; PF07645; EGF_CA; 11.
DR PROSITE; PS00010; ASX_HYDROXYL; 5.
DR PROSITE; PS01186; EGF_2; 5.
DR PROSITE; PS00026; EGF_3; 4.
DR PROSITE; PS01187; EGF_CA; 10.
KW EGF-like domain.
FT NON TER
FT NON TER
SQ SEQUENCE 823 AA; 90711 MW; 8E8CDA78DD291E1F CRC64;

Query Match      56.4%; Score 44; DB 2; Length 823;
Best Local Similarity 57.1%; Pred. No. 45;
Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 RQRLPKRMGGSYR 14
Db 14 KERTPKLEGTYR 26

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RT Bradyrhizobium japonicum USDA110.;

RL DNA Res. 9:189-197(2002).

DR EMBL, AP005935; BAC45342.1; -

DR GO: GO:0003824; F: catalytic activity; IEA.

DR GO: GO:0009116; P: nucleoside metabolism; IEA.

DR InterPro; IPR003615; HNH nuc.

DR InterPro; IPR000845; PNP UDP.

DR Pfam; PF01048; PNP_UDP_1_1.

DR SMART; SM00507; HNHc; I.

KW complete proteome.

SO SEQUENCE 474 AA; 52343 MW; 9537C1AE90B07BB4 CRC64;

Query Match 53.8%; Score 42; DB 2; Length 474;

Best Local Similarity 61.5%; Pred. No. 59;

Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 RORLPKRMGGSYR 13

DB 169 RGTIPTRGGSYR 181

RESULT 12

Q6GNB3 PRELIMINARY; PRT; 722 AA.

ID Q6GNB3

AC Q6GNB3

DT 05-JUL-2004 (TrEMBLrel. 27, Created)

DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)

DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)

DE MGC82906 protein.

GN Names=MGC82906;

OS Xenopus laevis (African clawed frog).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;

OC Xenopodinae; Xenopus.

OC NCBI_TaxID=8355;

RP [1]

RN SEQUENCE FROM N.A.

RC TISSUE=Spleen;

RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Donald M.P., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

RA Krzywinski M.I., Skalska U., Smaluk D.E., Schnerch A., Schein J.E.,

RA Jones S.J., Marra M.A.;

RT "Generation and initial analysis of more than 15,000 full-length human

RT and mouse cDNA sequences.;"

RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

RN [2]

RC SEQUENCE FROM N.A.

RP TISSUE=Spleen;

RC TISSUE=Spleen;

RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;

RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,

RA Richardson P.;

RA "Genetic and genomic tools for Xenopus research: The NIH Xenopus

RT initiative.;"

RL Dev. Dyn. 225:384-391(2002).

RN [3]

RP SEQUENCE FROM N.A.

RC TISSUE=Spleen;

RA Klein S., Gerhard D.S.;

RL Submitted (JUN-2004) to the EMBL/GenBank/DBAI databases.

QW	Complete proteome; GTP-binding; Initiation factor;	QW	Complete proteome; GTP-binding; Initiation factor;
FT	Protein biosynthesis.	FT	Protein biosynthesis.
FT	DOMAIN 664 816	FT	DOMAIN 664 816
FT	NP_BIND 670 677	FT	NP_BIND 670 677
FT	NP_BIND 720 724	FT	NP_BIND 720 724
FT	NP_BIND 774 777	FT	NP_BIND 774 777
QW	SEQUENCE 1169 AA; 127147 MW; 0705D909F5377562 CRC64;	QW	SEQUENCE 1169 AA; 127147 MW; 0705D909F5377562 CRC64;
Query Match	53.8%; Score 42; DB 1; Length 1169;	Query Match	52.8%; Score 41; DB 2; Length 83;
Best Local Similarity	61.5%; Pred. No. 1.5e+02;	Best Local Similarity	38.5%; Pred. No. 15;
Matches	8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;	Matches	5; Conservative 6; Mismatches 2; Indels 0; Gaps 0;
QY	1 RQLPKRMGGSYR 13	QY	2 RQLPKRMGGSYRC 14
DB	292 RQGVNREGGPR 304	DB	46 RNTAKLGGNFR 58
RESULT 14		RESULT 15	
ID	Q8YU7 PRELIMINARY; PRT; 83 AA.	ID	Q7UES8 PRELIMINARY; PRT; 384 AA.
AC	Q8YU7;	AC	Q7UES8;
DT	01-MAR-2002 (TrEMBLrel. 20, Created)	DT	01-OCT-2003 (TrEMBLrel. 25, Created)
DT	01-MAR-2002 (TrEMBLrel. 20, Last sequence update)	DT	01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT	01-OCT-2003 (TrEMBLrel. 25, Last annotation update)	DT	01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE	Asr0358 protein.	DE	Hypothetical protein.
GN	OrderedLocuNames=asr0358;	GN	OrderedLocuNames=RB10581;
OS	Anabaena sp. (strain PCC 7120).	OS	Rhodospirillum rubrum.
OC	Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.	OC	Bacteria; Planctomycetes; Planctomycetacia; Planctomycetales;
OX	NCBI_TaxID=103690;	OX	NCBI_TaxID=117;
RN	[1].	RN	[1].
RP	SEQUENCE FROM N.A.	RP	SEQUENCE FROM N.A.
RX	MEDLINE=21595285; PubMed=11759840;	RX	MEDLINE=22735913; PubMed=12835416; DOI=10.1073/pnas.1431443100;
RA	Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S.,	RA	Watanabe A., Iriguchi M., Iehikawa A., Kawashima K., Kimura T.,
RA	Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A.,	RA	Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A.,
RA	Nakazaki N., Shimpou S., Sugimoto M., Takazawa M., Yamada M.,	RA	Nakazaki N., Shimpou S., Sugimoto M., Takazawa M., Yamada M.,
RA	Yasuda M., Tabata S.;	RA	Yasuda M., Tabata S.;
RT	"Complete genomic sequence of the filamentous nitrogen-fixing	RT	"Complete genomic sequence of the filamentous nitrogen-fixing
RT	Cyanobacterium Anabaena sp. strain PCC 7120."	RT	Cyanobacterium Anabaena sp. strain PCC 7120."
RL	DNA Res. 8:1205-213(2001).	RL	DNA Res. 8:1205-213(2001).
DR	ENBL; AP003582; BAB72316.1; -.	DR	ENBL; AP003582; BAB72316.1; -.
DR	PIR; AE1851; AE1851.	DR	PIR; AE1851; AE1851.
DR	GO; GO:0005524; P:ATP binding; IEA.	DR	GO; GO:0005524; P:ATP binding; IEA.
DR	Pfam; PF02518; HATPase_c; 1.	DR	Pfam; PF02518; HATPase_c; 1.
KW	Complete proteome.	KW	Complete proteome.
QW	SEQUENCE 83 AA; 9321 MW; B315C9D52BDA04EC CRC64;	QW	SEQUENCE 83 AA; 9321 MW; B315C9D52BDA04EC CRC64;
Query Match	52.8%; Score 41; DB 2; Length 83;	Query Match	52.8%; Score 41; DB 2; Length 83;
Best Local Similarity	38.5%; Pred. No. 15;	Best Local Similarity	38.5%; Pred. No. 15;
Matches	5; Conservative 6; Mismatches 2; Indels 0; Gaps 0;	Matches	5; Conservative 6; Mismatches 2; Indels 0; Gaps 0;
QY	2 RQLPKRMGGSYRC 14	QY	2 RQLPKRMGGSYRC 14
DB	46 RNTAKLGGNFR 58	DB	46 RNTAKLGGNFR 58
RESULT 15		RESULT 15	
ID	Q7UES8 PRELIMINARY; PRT; 384 AA.	ID	Q7UES8 PRELIMINARY; PRT; 384 AA.
AC	Q7UES8;	AC	Q7UES8;
DT	01-OCT-2003 (TrEMBLrel. 25, Created)	DT	01-OCT-2003 (TrEMBLrel. 25, Created)
DT	01-OCT-2003 (TrEMBLrel. 25, Last sequence update)	DT	01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT	01-MAR-2004 (TrEMBLrel. 26, Last annotation update)	DT	01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE	Hypothetical protein.	DE	Hypothetical protein.
GN	OrderedLocuNames=RB10581;	GN	OrderedLocuNames=RB10581;
OS	Rhodospirillum rubrum.	OS	Rhodospirillum rubrum.
OC	Bacteria; Planctomycetes; Planctomycetacia; Planctomycetales;	OC	Bacteria; Planctomycetes; Planctomycetacia; Planctomycetales;
OC	Planctomycetacia; Planctomycetales;	OC	Planctomycetacia; Planctomycetales;
OX	NCBI_TaxID=117;	OX	NCBI_TaxID=117;
RN	[1].	RN	[1].
RP	SEQUENCE FROM N.A.	RP	SEQUENCE FROM N.A.
RT	STRAIN=1;	RT	STRAIN=1;
RX	MEDLINE=22735913; PubMed=12835416; DOI=10.1073/pnas.1431443100;	RX	MEDLINE=22735913; PubMed=12835416; DOI=10.1073/pnas.1431443100;

Search completed: November 18, 2005, 00:29:20
Job time : 87 secs

Result No.	Score	Query Match	\$	DB	ID	Description
1	45	57.7	433	4	US-09-252-991A-28695	Sequence 28695, A
2	43	55.1	164	4	US-09-252-991A-20615	Sequence 20615, A
3	43	55.1	164	4	US-09-252-991A-30154	Sequence 30154, A
4	43	55.1	223	4	US-09-252-991A-18819	Sequence 18819, A
5	43	55.1	243	4	US-09-252-991A-30417	Sequence 30417, A
6	42.5	54.5	1107	4	US-09-489-039A-8890	Sequence 8890, A
7	42	53.8	30	4	US-09-205-258-1167	Sequence 1167, Ap
8	42	53.8	419	4	US-09-252-991A-17499	Sequence 17499, A
9	41.5	53.2	381	4	US-09-502-540-11854	Sequence 11854, A
10	41	52.6	492	4	US-09-252-991A-20531	Sequence 20531, A
11	41	52.6	511	4	US-09-252-991A-18691	Sequence 18691, A
12	41	52.6	586	4	US-09-252-991A-22588	Sequence 22588, A
13	41	52.6	595	4	US-09-252-991A-17469	Sequence 17469, A
14	40	51.3	303	4	US-09-252-991A-22757	Sequence 22757, A
15	40	51.3	355	4	US-09-252-991A-37426	Sequence 37426, A
16	40	51.3	362	4	US-09-252-991A-30626	Sequence 30626, A
17	40	51.3	419	4	US-09-252-991A-28487	Sequence 28487, A
18	40	51.3	422	4	US-09-252-991A-18660	Sequence 18660, A
19	40	51.3	518	4	US-09-252-991A-25967	Sequence 25967, A
20	40	51.3	939	4	US-09-540-236-2399	Sequence 2399, Ap
21	39	50.0	232	4	US-09-489-039A-10126	Sequence 10126, A
22	39	50.0	542	1	US-08-412-431-3	Sequence 3, Appli
23	39	50.0	542	1	US-08-623-679-3	Sequence 3, Appli
24	39	50.0	542	3	US-08-933-774-3	Sequence 3, Appli
25	39	50.0	542	3	US-09-181-030-3	Sequence 3, Appli
26	39	50.0	542	3	US-09-534-242-3	Sequence 3, Appli
27	39	50.0	542	3	US-09-454-854-3	Sequence 3, Appli

EARLIER APPLICATION NUMBER: 60/048,895
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/049,375
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,891
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,880
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,896
EARLIER FILING DATE: 1997-06-06
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EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,876
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,895
EARLIER FILING DATE: 1997-06-06
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EARLIER FILING DATE: 1997-06-06
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EARLIER APPLICATION NUMBER: 60/048,882
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,899
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EARLIER APPLICATION NUMBER: 60/048,900
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EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/049,019
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,970
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,972
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,916
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/049,373
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,875
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/049,374
EARLIER FILING DATE: 1997-06-06
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EARLIER FILING DATE: 1997-06-06
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EARLIER APPLICATION NUMBER: 60/048,974
EARLIER FILING DATE: 1997-06-06
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EARLIER FILING DATE: 1997-06-06
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EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,898
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,962
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,963
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,877
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,878
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/070,923

EARLIER FILING DATE: 1997-12-18
EARLIER APPLICATION NUMBER: 60/092,921
EARLIER FILING DATE: 1998-07-15
EARLIER APPLICATION NUMBER: 60/094,657
EARLIER FILING DATE: 1998-07-30
NUMBER OF SEQ ID NOS: 1227
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1167
LENGTH: 30
TYPE: PRT
ORGANISM: Homo sapiens
US-09-205-258-1167

Query Match 53.8%; Score 42; DB 4; Length 30;
Best Local Similarity 61.5%; Pred. No. 1.1;
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 RORLPKRMGGSYR 13
DB 5 RORRPRRGGTGR 17

RESULT 8
US-09-252-991A-17499
Sequence 17499, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 17499
LENGTH: 419
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-17499

Query Match 53.8%; Score 42; DB 4; Length 419;
Best Local Similarity 60.0%; Pred. No. 19;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 5 PRMGGSYRC 14
DB 359 PRSGGFRRC 368

RESULT 9
US-09-902-540-11854
Sequence 11854, Application US/09902540
Patent No. 6833447
GENERAL INFORMATION:
APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Wiegand, Roger C.
TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
FILE REFERENCE: 38-10(15849)B
CURRENT APPLICATION NUMBER: US/09/902,540
CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: 60/217,883
PRIOR FILING DATE: 2000-07-10
NUMBER OF SEQ ID NOS: 16825
SEQ ID NO 11854
LENGTH: 381
TYPE: PRT
ORGANISM: Myxococcus xanthus

US-09-902-540-11854

Query Match 53.2%; Score 41.5; DB 4; Length 381;
Best Local Similarity 50.0%; Pred. No. 22;
Matches 10; Conservative 2; Mismatches 1; Indels 7; Gaps 1;

Qy 1 RQRLPKRMGG-----SYR 13
|:|||||
Db 113 RKSLPQRMGGALIGRWVSyr 132

RESULT 10

US-09-252-991A-20531
; Sequence 20531, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 20531
; LENGTH: 492
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
; NAME/KEY: UNSURE
; FEATURE: (313)
; LOCATION: (313)
; OTHER INFORMATION: Identity of amino acid at the above locations are unknown.
US-09-252-991A-20531

Query Match 52.6%; Score 41; DB 4; Length 492;
Best Local Similarity 50.0%; Pred. No. 35;
Matches 8; Conservative 3; Mismatches 1; Indels 4; Gaps 1;

Qy 3 RLPKRMGGSY----RC 14
|:|||||
Db 361 RLPRRLGGDHPRPVRC 376

RESULT 11

US-09-252-991A-18691
; Sequence 18691, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 18691
; LENGTH: 511
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-18691

Query Match 52.6%; Score 41; DB 4; Length 511;
Best Local Similarity 63.6%; Pred. No. 36;
Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 2 QRLPKRMGGSY 12

Db 492 KRLPKXSGSH 502
:|||||:|

RESULT 12

US-09-252-991A-22588
; Sequence 22588, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 22588
; LENGTH: 556
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-22588

Query Match 52.6%; Score 41; DB 4; Length 556;
Best Local Similarity 63.6%; Pred. No. 40;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 3 RLPKRMGGSYR 13
|:|||||
Db 420 RLPRRLGGQR 430

RESULT 13

US-09-252-991A-17469
; Sequence 17469, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 17469
; LENGTH: 595
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-17469

Query Match 52.6%; Score 41; DB 4; Length 595;
Best Local Similarity 70.0%; Pred. No. 43;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 5 PKRMGGSYRC 14
|:|||||
Db 38 PRSGGSARC 47

RESULT 14

US-09-252-991A-22757
; Sequence 22757, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

; FILE REFERENCE: 107196.136

; CURRENT APPLICATION NUMBER: US/09/252,991A

; CURRENT FILING DATE: 1999-02-18

; PRIOR APPLICATION NUMBER: US 60/074,788

; PRIOR FILING DATE: 1998-02-18

; PRIOR APPLICATION NUMBER: US 60/094,190

; PRIOR FILING DATE: 1998-07-27

; NUMBER OF SEQ ID NOS: 33142

; SEQ ID NO 22757

; LENGTH: 303

; TYPE: PRT

; ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-22757

Query Match

Best Local Similarity 51.3%; Score 40; DB 4; Length 303;

Matches 8; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 1 RORLPKRMGGSYRC 14

Db 61 RORLPKRMGGSYRC 74

RESULT 15

US-09-252-991A-27426

; Sequence 27426; Application US/09252991A

; Patent No. 6551795

; GENERAL INFORMATION:

; APPLICANT: Marc J. Rubenfield et al.

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

; FILE REFERENCE: 107196.136

; CURRENT APPLICATION NUMBER: US/09/252,991A

; CURRENT FILING DATE: 1999-02-18

; PRIOR APPLICATION NUMBER: US 60/074,788

; PRIOR FILING DATE: 1998-02-18

; PRIOR APPLICATION NUMBER: US 60/094,190

; PRIOR FILING DATE: 1998-07-27

; NUMBER OF SEQ ID NOS: 33142

; SEQ ID NO 27426

; LENGTH: 355

; TYPE: PRT

; ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-27426

Query Match

Best Local Similarity 51.3%; Score 40; DB 4; Length 355;

Matches 6; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RORLPKRMGGSY 12

Db 103 RORLPKRMGGSY 114

Search completed: November 19, 2005, 01:59:10

Job time : 28 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 18, 2005, 00:29:25 ; Search time 73 Seconds
(without alignments)
80.243 Million cell updates/sec

Title: US-09-745-008-14

Perfect score: 78

Sequence: 1 RQLPKRMGGSYRC 14

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867879 seqs, 418409474 residues

Total number of hits satisfying chosen parameters: 1867879

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 100%

Database : Published Applications AA:*

1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
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6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*
10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
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16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep.*
17: /cgn2_6/ptodata/2/pubpaa/US10E_PUBCOMB.pep.*
18: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
19: /cgn2_6/ptodata/2/pubpaa/US11A_PUBCOMB.pep.*
20: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
21: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
22: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	78	100.0	14	9 US-09-745-008-14	Sequence 14, Appl
2	78	100.0	21	9 US-09-745-008-13	Sequence 13, Appl
3	78	100.0	1162	9 US-09-745-008-34	Sequence 34, Appl
4	67.5	86.5	45	9 US-09-745-008-12	Sequence 12, Appl
5	43	55.1	105	16 US-10-437-963-113983	Sequence 113983,
6	43	55.1	133	16 US-10-437-963-113836	Sequence 278836,
7	43	55.1	142	15 US-10-425-114-58669	Sequence 58669, A
8	43	55.1	155	15 US-10-425-114-51601	Sequence 51601, A
9	43	55.1	162	15 US-10-425-114-47458	Sequence 47458, A
10	43	55.1	164	15 US-10-425-114-39475	Sequence 39475, A
11	43	55.1	165	15 US-10-425-114-38751	Sequence 38751, A

12	43	55.1	165	15	US-10-425-114-44961	Sequence 44961, A
13	43	55.1	166	15	US-10-425-114-39600	Sequence 39600, A
14	43	55.1	166	15	US-10-425-114-60911	Sequence 60911, A
15	43	55.1	166	15	US-10-425-114-62444	Sequence 62444, A
16	43	55.1	169	15	US-10-425-114-67338	Sequence 67338, A
17	43	55.1	179	15	US-10-425-114-61006	Sequence 61006, A
18	43	55.1	179	15	US-10-425-114-62787	Sequence 62787, A
19	43	55.1	181	15	US-10-425-114-39542	Sequence 39542, A
20	43	55.1	181	15	US-10-425-114-72129	Sequence 72129, A
21	43	55.1	181	15	US-10-425-114-72143	Sequence 72143, A
22	43	55.1	183	15	US-10-425-114-58636	Sequence 58636, A
23	43	55.1	184	15	US-10-425-114-55429	Sequence 55429, A
24	43	55.1	185	15	US-10-425-114-47709	Sequence 47709, A
25	43	55.1	185	15	US-10-425-114-65756	Sequence 65756, A
26	42	53.8	30	10	US-09-933-767-1167	Sequence 1167, Ap
27	42	53.8	30	14	US-10-004-860-1167	Sequence 1167, Ap
28	42	53.8	30	14	US-10-023-282-1167	Sequence 1167, Ap
29	42	53.8	326	16	US-10-437-963-175186	Sequence 175186,
30	42	53.8	339	20	US-11-097-143-32442	Sequence 32442, A
31	41	52.6	208	16	US-10-437-963-176745	Sequence 176745,
32	41	52.6	337	16	US-10-437-963-143589	Sequence 143589,
33	41	52.6	524	16	US-10-739-930-10355	Sequence 10355, A
34	41	52.6	564	15	US-10-369-493-585	Sequence 585, App
35	40.5	51.9	235	14	US-10-240-154-22	Sequence 22, Appl
36	40.5	51.9	748	16	US-10-437-963-115827	Sequence 115827,
37	40	51.3	53	16	US-10-437-963-183455	Sequence 183455,
38	40	51.3	60	15	US-10-424-599-176730	Sequence 176730,
39	40	51.3	63	16	US-10-425-115-284352	Sequence 284352,
40	40	51.3	147	15	US-10-424-599-152415	Sequence 152415,
41	40	51.3	150	14	US-10-156-763-10416	Sequence 10416, A
42	40	51.3	151	18	US-10-450-763-47114	Sequence 47114, A
43	40	51.3	185	15	US-10-425-114-60116	Sequence 60116, A
44	40	51.3	230	9	US-09-741-669-372	Sequence 372, App
45	40	51.3	230	15	US-10-282-122A-42769	Sequence 42769, A

ALIGNMENTS

RESULT 1

US-09-745-008-14
; Sequence 14, Application US/09745008
; Patent No. US20020137667A1
; GENERAL INFORMATION:
; APPLICANT: Chuenkova, Marina
; APPLICANT: Pereira, Mircio A.
; TITLE OF INVENTION: T. Cruci-Derived Neurotrophic Agents and
; TITLE OF INVENTION: Methods of Use Therefor
; FILE REFERENCE: 1322.1028-001
; CURRENT APPLICATION NUMBER: US/09/745,008
; CURRENT FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: US 60/172,881
; PRIOR FILING DATE: 1999-12-20
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
US-09-745-008-14

Query Match 100.0%; Score 78; DB 9; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.5e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RQLPKRMGGSYRC 14

DB 1 RQLPKRMGGSYRC 14

RESULT 2

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US-09-745-008-13
; Sequence 13, Application US/09745008
; Patent No. US20020137667A1
; GENERAL INFORMATION:
; APPLICANT: Chuenkova, Marina
; APPLICANT: Pereira, Mircio A.
; TITLE OF INVENTION: T. Cruzi-Derived Neurotrophic Agents and
; TITLE OF INVENTION: Methods of Use Therefor
; FILE REFERENCE: 1322.1028-001
; CURRENT APPLICATION NUMBER: US/09/745,008
; CURRENT FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: US 60/172,881
; PRIOR FILING DATE: 1999-12-20
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
US-09-745-008-13

Query Match      100.0%; Score 78; DB 9; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.8e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RQLPKRMGGSYRC 14
| | | | | | | | | |
Db 1 RQLPKRMGGSYRC 14

RESULT 3
US-09-745-008-34
; Sequence 34, Application US/09745008
; Patent No. US20020137667A1
; GENERAL INFORMATION:
; APPLICANT: Chuenkova, Marina
; APPLICANT: Pereira, Mircio A.
; TITLE OF INVENTION: T. Cruzi-Derived Neurotrophic Agents and
; TITLE OF INVENTION: Methods of Use Therefor
; FILE REFERENCE: 1322.1028-001
; CURRENT APPLICATION NUMBER: US/09/745,008
; CURRENT FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: US 60/172,881
; PRIOR FILING DATE: 1999-12-20
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 34
; LENGTH: 1162
; TYPE: PRT
; ORGANISM: Trypanosoma cruzi
US-09-745-008-34

Query Match      100.0%; Score 78; DB 9; Length 1162;
Best Local Similarity 100.0%; Pred. No. 0.0002;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RQLPKRMGGSYRC 14
| | | | | | | | | |
Db 379 RQLPKRMGGSYRC 392

RESULT 4
US-09-745-008-12
; Sequence 12, Application US/09745008
; Patent No. US20020137667A1
; GENERAL INFORMATION:
; APPLICANT: Chuenkova, Marina
; APPLICANT: Pereira, Mircio A.
; TITLE OF INVENTION: T. Cruzi-Derived Neurotrophic Agents and
; TITLE OF INVENTION: Methods of Use Therefor
; FILE REFERENCE: 1322.1028-001
; CURRENT APPLICATION NUMBER: US/09/745,008
; CURRENT FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: US 60/172,881
; PRIOR FILING DATE: 1999-12-20
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 45
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
US-09-745-008-12

Query Match      86.5%; Score 67.5; DB 9; Length 45;
Best Local Similarity 93.3%; Pred. No. 0.00051;
Matches 14; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 1 RQLPKRMGGSYRC 14
| | | | | | | | | |
Db 24 RQLPKRMGGSYRC 38

RESULT 5
US-10-437-963-113983
; Sequence 113983, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 113983
; LENGTH: 105
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_17719C.1.pep
US-10-437-963-113983

Query Match      55.1%; Score 43; DB 16; Length 105;
Best Local Similarity 64.3%; Pred. No. 19;
Matches 9; Conservative 1; Mismatches 2; Indels 2; Gaps 1;

Qy 3 RLPK--RMGGSYRC 14
| | | | | | | | | |
Db 63 RLPRVSRGGPYRC 76

RESULT 6
US-10-425-115-278836
; Sequence 278836, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
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; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 278836
; LENGTH: 133
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_185877C.1.pap
US-10-425-115-278836

Query Match 55.1%; Score 43; DB 16; Length 133;
Best Local Similarity 60.0%; Pred. No. 25;
Matches 9; Conservative 2; Mismatches 2; Indels 2; Gaps 1;

QY 2 ORLP--KRMGGSYRC 14
||| :|||
Db 107 QRCFNNRRLGSLRC 121

RESULT 7

US-10-425-114-58669
; Sequence 58669, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 58669
; LENGTH: 142
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 700615246_FLI.pap
US-10-425-114-58669

Query Match 55.1%; Score 43; DB 15; Length 142;
Best Local Similarity 70.0%; Pred. No. 26;
Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 RORLPKRMGG 10
:|||||
Db 108 RRRLPRLGG 117

RESULT 8

US-10-425-114-51601
; Sequence 51601, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 51601
; LENGTH: 155
; TYPE: PRT
; ORGANISM: Zea mays

; FEATURE:
; OTHER INFORMATION: Clone ID: 700222827_FLI.pap
US-10-425-114-51601

Query Match 55.1%; Score 43; DB 15; Length 155;
Best Local Similarity 70.0%; Pred. No. 29;
Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 RORLPKRMGG 10
:|||||
Db 133 RRRLPRLGG 142

RESULT 9

US-10-425-114-47458
; Sequence 47458, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 47458
; LENGTH: 162
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 700106619_FLI.pap
US-10-425-114-47458

Query Match 55.1%; Score 43; DB 15; Length 162;
Best Local Similarity 70.0%; Pred. No. 30;
Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 RORLPKRMGG 10
:|||||
Db 133 RRRLPRLGG 142

RESULT 10

US-10-425-114-39475
; Sequence 39475, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 39475
; LENGTH: 164
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 700207896_FLI.pap
US-10-425-114-39475

Query Match 55.1%; Score 43; DB 15; Length 164;

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Best Local Similarity 70.0%; Pred. No. 30;
Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RORLPKRMGG 10
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Db 108 RRRLPRLGG 117

RESULT 11
US-10-425-114-38751
; Sequence 38751, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 38751
; LENGTH: 165
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: UC-ZMFLB73069E07_FLI.pep
US-10-425-114-38751

Query Match 55.1%; Score 43; DB 15; Length 165;
Best Local Similarity 70.0%; Pred. No. 30;
Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RORLPKRMGG 10
|:||||:|
Db 108 RRRLPRLGG 117

RESULT 12
US-10-425-114-44961
; Sequence 44961, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 44961
; LENGTH: 165
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 700448317_FLI.pep
US-10-425-114-44961

Query Match 55.1%; Score 43; DB 15; Length 165;
Best Local Similarity 70.0%; Pred. No. 30;
Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RORLPKRMGG 10
|:||||:|

Best Local Similarity 70.0%; Pred. No. 31;
Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Db 108 RRRLPRLGG 117

RESULT 13
US-10-425-114-39600
; Sequence 39600, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 39600
; LENGTH: 166
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 700442376_FLI.pep
US-10-425-114-39600

Query Match 55.1%; Score 43; DB 15; Length 166;
Best Local Similarity 70.0%; Pred. No. 31;
Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RORLPKRMGG 10
|:||||:|
Db 108 RRRLPRLGG 117

RESULT 14
US-10-425-114-60911
; Sequence 60911, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 60911
; LENGTH: 166
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3354-104-B1_FLI.pep
US-10-425-114-60911

Query Match 55.1%; Score 43; DB 15; Length 166;
Best Local Similarity 70.0%; Pred. No. 31;
Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RORLPKRMGG 10
|:||||:|
Db 108 RRRLPRLGG 117

RESULT 15
US-10-425-114-62444
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; Sequence 62444, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 62444
; LENGTH: 166
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 700578933_FLI.pep
US-10-425-114-62444

Query Match      55.1%; Score 43; DB 15; Length 166;
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Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      1 RORLPKRMGG 10
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Db      108 RRRLPRRLGG 117

Search completed: November 19, 2005, 02:04:42
Job time : 76 secs

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